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US-09-791-118A-1

US-10-232-188-4

US-10-133-628-11

US-10-732-923-13341

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US-10-732-923-13342

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RESULT 1
US-09-791-118A-3
; Sequence 3, Application US/09791118A
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; Patent No. US20020034741A1
; GENERAL INFORMATION:
APPLICANT: Braun, Susanne
; APPLICANT: Pentaberg, Jorn-Peter
APPLICANT: Regenbogen, Johannes
; TITLE OF INVENTION: Use of polypeptides or nucleic acids
TITLE OF INVENTION: Use of polypeptides or nucleic acids
TITLE OF INVENTION: Leatment of skin or intestinal disorders,
TITLE OF INVENTION: the identification of pharmacologically
TITLE OF INVENTION: active substances
; TITLE OF INVENTION: DATE: 2001-02-22
; CURRENT APPLICATION NUMBER: US/09/791,118A
; CURRENT FILING DATE: 2000-04-24
; PRIOR FILING DATE: 2000-04-24
; PRIOR FILING DATE: 2000-04-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.5e-82;
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US-10-232-188-5
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Publication No. US20030207830A1
GENERAL INFORMATION:
APPLICANT: GALLOIS-MONTBRUN, SARAH
APPLICANT: GIACOMONI-FERNANDES, VERONIQUE
APPLICANT: GIACOMONI-FERNANDES, VERONIQUE
APPLICANT: DEVILLE-BONNE, DOMINIQUE
APPLICANT: VERON, MICHEL
TITLE OF INVENTION: MUTANT NDP KINASES FOR ANTIVIRAL NUCLEOTIDE ANTITLE OF INVENTION: ACTIVATION AND THERAPEUTIC USES THEREOF
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                                  APPLICANT: Bandman, Olga
Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                         Inc
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1.5e-82;
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEFAX: 415-845-4166
FORMATION FOR SEQ ID NO: 5:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,188
FILING DATE: 28-Aug-2002
PRIOR APPLICATION NUMBER: US/08/713,825
                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
CITY: Palo Alto
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CLONE: 127983
SEQUENCE DESCRIPTION: SEQ ID NO:
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SEQUENCE CHARACTERISTICS
LENGTH: 152 amino acid
Publication No. US20030022306A1
GENERAL INFORMATION:
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APPLICANT: O'FARRELL, ANNE-MARIE
APPLICANT: WORIMOTO, ALYSSA
APPLICANT: SMOLICH, BEVERLY
APPLICANT: MALTER, SALAH
APPLICANT: WALTER, SALAH
APPLICANT: CHERRINGTON, JULIE
APPLICANT: CHERRINGTON, JULIE
APPLICANT: CHERRINGTON, JULIE
APPLICANT: CHERRINGTON, JUN
TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
FILE REFERENCE: 038602/1592
CURRENT APPLICATION NUMBER: 60/380,872
PRIOR APPLICATION NUMBER: 60/380,872
PRIOR FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 185
SOFTWARE: Patentin Ver: 2.1
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Pred. No. 1.5e-82;
); Mismatches 0;
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Pred. No. 1.5e-82;
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FILE REFERENCE: 03495.022/-uvvv
CURRENT APPLICATION NUMBER: US/10/133,628
CURRENT FILING DATE: 2002-04-29
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 152
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Publication No. US20040018528A1
GENERAL INFORMATION:
APPLICANT: DEPRIMO, SAMUEL
APPLICANT: O'FARRELL, ANNE-MARIE
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SEQ ID NO 90
LENGTH: 152
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ilarity 99.3%;
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151; Conser
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LENGTH: 152
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Sequence 13346, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
                                                                                                                                  PLANTS WITH IMPROVED PHENOTYPES
                                                                                                                                                                                                                                                                                                          Length 152
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Pred. No. 5.3e-82
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                                                        US-10-732-923-13345
; Sequence 13345, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH I
FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13345
; LENGTH: 152
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Pred. No.
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PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 13346
LENGTH: 151
TYPE: PRT
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APPLICANT: SCHNEIDER, BENOIT
APPLICANT: SCHNEIDER, BENOIT
APPLICANT: GIACOMONI-FERNANDES, VERONIQUE
APPLICANT: GIACOMONI-FERNANDES, VERONIQUE
APPLICANT: DEVILLE-BONNE, DOMINIQUE
TITLE OF INVENTION: MUTANT NDP KINASES FOR ANTIVIRAL NUCLEOTIDE ANALOG
TITLE OF INVENTION: ACTIVATION AND THERAPEUTIC USES THEREOF
FILE REFERENCE: 03495.0227-00000
CURRENT APPLICATION NUMBER: US/10/133,628
CURRENT APPLICATION NUMBER: US/10/133,628
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN Ver. 2.1
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US-11-013-684-1
Sequence 1, Application US/11013684
Publication No. US20050136489A1
GENERAL INFORMATION:
APPLICANT: Industrial Technology Research Institute
TITLE OF INVENTION: Biomakers for Liver Diseases and Method for Using
FILE REFERENCE: 04P0019
CURRENT APPLICATION NUMBER: US/11/013,684
CURRENT FILING DATE: 2004-12-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.2
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Pred. No. 5.3e-82;
Mismatches 0;
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Pred. No. 5.4e-82
L; Mismatches
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Publication No. US20030207830Al
GENERAL INFORMATION:
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Patent No. US20020034
GENERAL INFORMATION:
APPLICANT: Werner, San APPLICANT: Braun, St
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SEQ ID NO 4
LENGTH: 152
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APPLICANT: Jackson, Christina M.; Dufour, Gerard E.;
APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
APPLICANT: Ones, Anissa L.; Yu, Jimmy Y.;
APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Gerstin,Jr., Edward H.; Peralta, Careyna H.;
APPLICANT: Gerstin,Jr., Edward H.; Penzer, Scott R.;
APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Inman, Rebekah R.
TILE OF INVENTION WOLECULES FOR DISEASE DETECTION AND TREATMENT
FILE REFERENCE: PT-1183 USN
CURRENT APPLICATION NUMBER: US/10/363,829
CURRENT FILING DATE: 2003-03-05
PRIOR FILING DATE: 2001-09-05
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,751
PRIOR APPLICATION NUMBER: US 60/229,749
FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRS
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Sequence 13127, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
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Pred. No. 1.5e-81;
2; Mismatches 1;
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; Sequence 352, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
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Best Local Similarity 98.0%;
Matches 149; Conservative
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US-10-732-923-13127
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LENGTH: 152
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APPLICANT: Perabelly Substances
APPLICANT: Perabergy Journ-Peter
APPLICANT: Goppelt, Andreas
APPLICANT: Regenbogen, Johannes
TITLE OF INVENTION: Use of polypeptides or nucleic acids
TITLE OF INVENTION: encoding these of the gene family NM23 for the diagnosis or
TITLE OF INVENTION: treatment of skin or intestinal disorders, and their use for
TITLE OF INVENTION: active substances
TITLE OF INVENTION: do 102-22
TITLE OF INVENTION NUMBER: US 60/199,312
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: Incyte ID No: LG:1098570.1.orf3:2000SEP08
US-10-363-829-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 190;
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Pred. No. 2e-81;
2; Mismatches
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DR APPLICATION NUMBER: US 60/229,750
DR FILING DATE: 2000-09-05
DR APPLICATION NUMBER: US 60/229,747
DR FILING DATE: 2000-09-05
DR APPLICATION NUMBER: US 60/229,748
DR FILING DATE: 2000-09-05
DR APPLICATION NUMBER: US 60/230,583
DR FILING DATE: 2000-09-05
DR FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-09-06
ling Prior Application data removed
t OF SEQ ID NOS: 506
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Best Local Similarity 98.0%;
Matches 149; Conservative
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Susanne
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. US20020034741A1
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Remaining Prior AFF...
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PERL Program
SEQ ID NO 352
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                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10133628

Sequence 5, Application US/10133628

Sequence 5. Application US/20030207830A1

GENERAL INFORMATION:

APPLICANT: GALLOIS-MONTBRUN, SARAH

APPLICANT: GIACOMONI-FERNANDES, VERONIQUE

APPLICANT: DEVILLE-BONNE, DOMINIQUE

APPLICANT: DEVILLE-BONNE, DOMINIQUE

APPLICANT: VERON, MICHEL

TITLE OF INVENTION: MUTANT NDP KINASES FOR ANTIVIRAL NUCLEOTIDE ANAI

TITLE OF INVENTION: ACTIVATION AND THERAPEUTIC USES THEREOF

FILE REFERENCE: 03495.0227-00000

CURRENT FILING DATE: 2002-04-29

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTIN VEY: 2.1

SEQ ID NO 5

LENGTH: 152
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US-10-732-923-13128
; Sequence 13128, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
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Pred. No. 3.3e-81
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                                                              Score 793; DB 5
Pred. No. 2e-81;
; Mismatches
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nilarity 98.7%;
Conservative
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ORGANISM: Artificial Sequence
                                                              98.8%;
larity 98.0%;
Conservative

; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-732-923-13113
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Best Local Similarity
Matches 150; Conser
                                                                            ul Similarity
149; Conser
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US-10-133-628-5
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-10-133-628-5
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Best Local
Matches 14
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                                      Gaps
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Sequence 332, Application US/10116275

Publication No. US20030211476A1

GENERAL INFORMATION:

APPLICANT: Elan Pharmaceutical Technology

APPLICANT: Brayden, David

APPLICANT: Brayden, David

APPLICANT: Hambkin, Imelda

APPLICANT: Higgins, Lisa

TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells an

TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cell;

FILE REFERENCE: E1067/20087

CURRENT FILING DATE: 2002-10-04

NUMBER OF SEQ ID NOS: 349

SOFTWARE: PatentIn version 3.1

SEQ ID NO 332

LENGTH: 152
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US-10-732-923-13113
US-10-732-923-13113; Application US/10732923
; Sequence 13113, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT PILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13113
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             Score 793; DB 3 Pred. No. 2e-81;
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Pred. No. 2e-81;
2; Mismatches
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                                      Mismatches
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Conservative
          98.8%;
ilarity 98.0%;
Conservative
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149; Conser
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             Query Match
Best Local S
Matches 149
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Pred. No. 9.5e-81;
2; Mismatches 2;
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; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13128
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-13128
                                                                                                                                                                                                                                                                                                                                     Search completed: December 16, 2005, 17:01:37 Job time : 108.547 secs
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                                                                                                                                 Query Match
Best Local Similarity 97.4%;
Matches 148; Conservative
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Compugen Ltd
GenCore version (c) 1993 - 2005
          Copyright
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conds Sec 16:39:14 2005, December 16, on: Run

es/sec updat ; Search time 6.69182 (without alignments) 153.021 Million cell up

US-10-074-694-5 Title:

803 score: Perfect

..WFKPEELVDYKSCAHDWVYE MANLERTFIAIKPDGVQRGL Sequence:

Gapext BLOSUM62 Gapop 10.0 Scoring table:

residues 51470 segs, 6736768 Searched:

0.5

51470 chosen parameters satisfying hits of number Total

length: 0 length: 2000000000 sed sed Minimum DB Maximum DB Maximum Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Published Database

/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*/ Applications_AA_New:* 10 M 4 M 9 L 8

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. Pred. No score gand is

SUMMARIES

Description	Sequence 1577, Ap	, Ap	966, Ap	994,	10, A	equence 118, Ap	, Ap	equence 8, Apr	Sequence 3294, Ap	600, 7	equence 297	, 99	equence 3314,	308, A	equence 412, A	1218	42, Ap	e 326, Ap	3, App	Appl	96, App	Ap	2758, A	2	e 31, App
7 1	1-234-	78-556A-4	5-822-9	22-99	-411		-726-	0	-626-32	1-60	94-2	-626-26	3-626-	-822-30	-626-41	-626-12		n	US-10-451-375-3	Ĺ	US-11-074-176-96		US-10-467-657-2758		US-11-143-980-31
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equence 22	020,	34,	6, A	190, A	Sequence 240, App	, App	, Appl	92,	48, A	2, App	, App	58, A	00, A	8, AF	Sequence 1654, Ap	20, 4	4, Ap	, Ap	66, A
-11-074-176-22	6-2	7-4	17-	6-19	6-2	US/11/062	US/11/062	9-	-10-467-657-754	-11-090-4	US-10-510-386-26	-10-793-626-1	-10-467-657-82	-10-793-626-3	7-1	57-18	7-52	US-10-485-517-202	US-10-793-626-2066
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ALIGNMENTS

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                                                                                                                                                                 and Treatment of Preeclampsia
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US-10-878-556A-49
; Sequence 49, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 803; DB 6;
Pred. No. 1.1e-78;
; Mismatches 0;
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RESULT 1
US-10-821-234-1577

Sequence 1577, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

PRIOR PPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PL SEQ Genes Version 1.0

SEQ ID NO 1577

LENGTH: 152

TYPE: PRT

ORGANISM: Homo sapiens

US-10-821-234-1577
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                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Silarity 100.0%; P
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Best Local Similarity
Matches 152; Conser
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us-10-074-694-5.rapbn

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Publication No. US20050260707A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
                                                                                                                                                                                                                                Length 152;
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                                                                                                                                                                                                                              Score 720; DB 6; Pred. No. 7.5e-70; 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                     152
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                                                                                                                         CRGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw_hum/ndka_human
DATABASE ENTRY DATE: 1990-04-01
US-10-878-556A-49
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CURRENT APPLICATION NUMBER: US/11/055,82;
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-08
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CURRENT APPLICATION NUMBER: US/10/878, CURRENT FILING DATE: 2004-06-28 NUMBER OF SEQ ID NOS: 199
SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
LENGTH: 152
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1-055-822-966
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Remaining Prior Application data
NUMBER OF SEQ ID NOS: 1158
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                                                                                                                                                                                                                              / Match 89.7%;
Local Similarity 88.2%;
les 134; Conservative 10
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APPLICATION NUMBER: DE 1
FILING DATE: 1999-07-08
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US-11-055-822-966
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TH: 136
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Best Local S
Matches 134
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Dublication No. US20050260707A1

GENERAL INFORMATION:

APPLICANT: Pompejus, Markus

APPLICANT: Schroder, Hartwig

APPLICANT: Schroder, Hartwig

APPLICANT: APPLICANT: GCRYNEBACTERIUM GLUTAMICUM GENE

TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENE

TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS

FILE REFERENCE: BGI-121CPCN

CURRENT APPLICATION NUMBER: US/11/055,822

CURRENT APPLICATION NUMBER: 09/606,740

PRIOR PILING DATE: 1999-06-25

PRIOR PILING DATE: 1999-07-02

PRIOR FILING DATE: 1999-07-02

PRIOR PILING DATE: 1999-07-02

PRIOR PILING DATE: 1999-07-03

PRIOR PILING DATE: 1999-07-01

PRIOR PILING DATE: 1999-07-01

PRIOR PILING DATE: 1999-07-01

PRIOR PILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

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 Score 335.5; DB 7 Pred. No. 4.8e-29;
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Pred. No. 4.8e-29;
                                             Mismatches
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  41.8%;
llarity 50.4%;
Conservative 2
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                          Similarity 66; Conser
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TH: 136
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Best Local S
Matches 66
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                          Local
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36; Conser
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LENGTH: 795
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US-10-525-710-8
34;
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Best Local S
Matches 36
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 141;
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                                                                                                                                                                                                                           GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.2%; Score 307; DB 6;
larity 43.4%; Pred. No. 5.3e-26;
Conservative 27; Mismatches 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No. US20050266541A1
GENERAL INFORMATION:
APPLICANT: Solazyme, Inc.
APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: Production
FILE REFERENCE: H2042101-CIP
CURRENT APPLICATION NUMBER: US/10/763,712A
CURRENT FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: US 10/287,750
PRIOR FILING DATE: 2003-04-12
PRIOR FILING DATE: 2003-04-12
PRIOR FILING DATE: 2003-04-12
PRIOR FILING DATE: 2003-04-12
PRIOR FILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                         FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 4110
LENGTH: 141
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Pred. No.
                                                                                           Sequence 4110, Application US/10467657; Publication No. US20050260581A1; GENERAL INFORMATION:
APPLICANT: CHIRON SpA; APPLICANT: FONTANA Maria Rita; APPLICANT: PIZZA Mariagrazia; APPLICANT: MASIGNANI Vega; APPLICANT: MONACI Elisabetta; TITLE OF INVENTION: GONOCOCCAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 118, Application US/10763712A Publication No. US20050266541A1
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nes 59; Conser
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US-10-763-712A-118
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Best Local
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                                  61
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APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING,
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
                                                        81 LNVVKTGRVMLGETNPADSKPGTIR-GDFCIQVGRNIIHGSDSVKSAEKEISLWFKPEEL
                                                                                                                                              - FANNLAQAL
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                                 --RFEOKGFRLVAMKFLRASEEHLKOHYIDLKDRPFF
                                                                                                        PGLV-KYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
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GENERAL INFORMATION:
APPLICANT: Kroger, Burkhard
APPLICANT: Zelder, Oskar
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Hafner, Stefan
TITLE OF INVENTION: Method for Zymotic Production of Fin
TITLE OF INVENTION: Sulphur (metY)
FILE REFERENCE: 13111-00006-US
CURRENT APPLICATION NUMBER: US/10/525,710
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: PCT/EP 2003/009453
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Mismatches
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                                                                                                                                                                                                                                                                                                                 Sequence 49, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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                                  7 TFIAIKPDGVQRGLVGEIIK-
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CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 371
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: amino acid sequence
                                                                                                                                                                    4.9;
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Pred. No. 4
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                  082.7
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US-10-793-626-3294
; Sequence 3294, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
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Publication No. US20050272054A1
GENERAL INFORMATION:
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                   102
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PRIOR FILING DATE: ZVVZ DE 102
PRIOR APPLICATION NUMBER: DE 102
PRIOR FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.3
                                                                                                                                                        8.5%;
                                                                                                 ; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-525-710-8
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les 35; Conser
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Best Local S
Matches 35
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APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND METH
TITLE OF INVENTION: USE
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
               Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
DETECTION AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/11/194,246;
CURRENT FILING DATE: 2005-08-01;
PRIOR APPLICATION NUMBER: US/10/274,586;
PRIOR FILING DATE: 2002-10-21;
PRIOR APPLICATION NUMBER: US 60/345,438;
PRIOR FILING DATE: 2001-10-19;
NUMBER OF SEQ ID NOS: 621;
SOFTWARE: Patentin version 3.0;
LENGTH: 135;
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Pred. No. 52;
APPLICANT: CARGLLL,
TITLE OF INVENTION: GENETIC FOLLOWING TITLE OF INVENTION: DETECTION AND USES THER FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 600
TENGTH: 2261
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Pred. No.
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Publication No. US20050272089A1
GENERAL INFORMATION:
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LSRIIWKALKPLLVGKILYTPDTPA
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ilarity 23.5%;
Conservative 20
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ilarity 22.5%;
Conservative 1
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20; Conser
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US-10-793-626-2666
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Best Local S
Matches 23
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 B.1%; Score 65; DB (1 Darity 23.6%; Pred. No. 5.2; Conservative 16; Mismatches
                                                                                                                                                                                                                          of Artificial
                                                                                                                                                                                                                                                                                              8.2%; Score 65.5; I llarity 26.9%; Pred. No. 11; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3314, Application US/10793626; Publication No. US20050255478A1; GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMID; FILE REFERENCE: PU3480US; CURRENT APPLICATION NUMBER: US/10/793,626; CURRENT FILING DATE: 2004-03-04; PRIOR FILING DATE: 1999-11-09; NUMBER OF SEQ ID NOS: 4472; SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3314; LENGTH: 230
FILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT FILING DATE: 2004-03-04

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2666

LENGTH: 459
                                                                                                                                                                                                                        OTHER INFORMATION: Description of Arti
OTHER INFORMATION: amino acid sequence
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Publication No. US20050260707A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
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ORGANISM: Artificial Sequence
                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
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Mismatches
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; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIL
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR PPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 412
; LENGTH: 204
                                                                                                                                                           FILING DATE: 2000-06-23

OR APPLICATION NUMBER: 60/141,031

OR APPLICATION NUMBER: 60/142,101

OR FILING DATE: 1999-06-25

OR APPLICATION NUMBER: 60/148,613

OR APPLICATION NUMBER: 60/187,970

OR FILING DATE: 1999-08-12

OR APPLICATION NUMBER: 60/187,970

OR FILING DATE: 2000-03-09

OR APPLICATION NUMBER: DE 19930476.9

OR APPLICATION NUMBER: DE 19931415.2

OR APPLICATION NUMBER: DE 19931415.2

OR APPLICATION NUMBER: DE 19931418.7
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Remaining Prior Application data
NUMBER OF SEQ ID NOS: 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 1
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 1
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nes 32; Conser
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US-10-793-626-412
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US-10-793-626-412
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7.9%; Score 63.5; DB 6; Length 204; 21.4%; Pred. No. 6.4;	Compervative 20, mismacches 41, indeis 31, daps	GFRLVAMKFLRASEEHL	76 MLKRFKIETLFFVIVMSLSSTLNPLLKNIFD-RERPTLLRLIDISGFSFPSGHAMGSTSF 134	PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCI 110	135 FGSAIYVINRHDSGISKGVLIGLCALFILLISTSRVYLGVHYPTDIIAGIIGGVFCL 191
Simi		24 IIKRFEQKGFR	76 MLKRFKIETLF	61 FPGLVKYMN	35 FGSAIYVINRH
Query Match Best Local	HACCIES	δλ	qa	ολ	T qa

Search completed: December 16, 2005, 17:01:58 Job time : 7.69182 secs .rag

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Compugen Ltd.
version - 2005
GenCore (c) 1993
        Copyright
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sw model using protein search, OM protein

onds 16:31:59 2005, December 16, Run on:

es/sec update ; Search time 138.333 Sec (without alignments) 527.255 Million cell update

US-10-074-694-3 876 score: Title: Perfect

..WFQPEELVEYKSCAQNWIYE QSQPAVKPCHLKGTMANSER... Sequence:

166

BLOSUM62 Gapop 10.0 Scoring table:

0.5 Gapext -

residues 2443163 segs, 439378781 Searched:

hits satisfying chosen parameters of Total number

2000000000 length: length: seq seq DB DB Minimum Maximum . 100% . 45 summaries Maximum Match 1 Listing first Post-processing:

Database

A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
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inted, ಹ Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.

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No.	Score	Match	Length	BB :	QI	Description
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7	σ	0	8	4	AAM78984	98
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ALIGNMENTS

standard; protein; 152 entry) protein (first Murine NM23A 12-FEB-2002 AAG80281 RESULT 1

NM23; skin disease; intestinal disease; wound healing; vulnerary; ulcer; antitumour; gastrointestinal; dermatological; anti-inflammatory; tumour; antiulcer; nucleotide-diphosphate kinases; DNA-binding agent; psoriasis; transcription activating agent; Ras-GTPase regulator; Crohn's disease; NM23A; murine

Mus musculus.

EP1127576-A1

29-AUG-2001.

2001EP-00103624 22-FEB-2001; 23-FEB-2000; 2000DE-01008330 24-APR-2000; 2000US-0199312P

SWITCH BIOTECH AG. ETH ZUERICH ETH ZENT HOENGGERBERG (SWIT-) (ETHZ-)

Regenbogen Ą Goppelt ם, Halle Braun S, ŝ Werner

ŋ

WPI; 2001-490891/54

and for diagnosis, prevention, and in screening for for Use of NM23 polypeptide and nucleic acid, f treatment of skin and intestinal diseases, therapeutic agents.

48pp; German. Claim 1; Page 21-22; This invention describes a novel use of the NM23 protein family, for analysis, diagnosis, prevention and/or treatment of skin or intestinal diseases and/or wound healing and/or associated pathological disturbances. The products of the invention have vulnerary, antitumour, gastrointestinal, dermatological, anti-inflammatory and antiulcer activity. The NM23 protein family act as nucleotide-diphosphate kinases, activity, The NM23 protein family act as nucleotide-diphosphate kinases, buA-binding and transcription activating agents and regulators of Ras-

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       ected against transformed
GTPases. The proteins of the invention, antibodies (Ab) directed against them, and their encoding nucleic acids, or related vectors, transformed cells and antisense sequences, are used for analysis, diagnosis, prevention and/or treatment of skin and intestinal diseases (where associated with uncontrolled tissue growth or cell differentiation, particularly skin and intestinal tumours, also psoriasis, Crohn's diseas and ulcers), wound healing and/or associated pathological alterations). They are also used to screen for agents that are potentially useful for treating these conditions. In vitro monitoring of NM23 protein expression in tissue samples provides an early diagnosis of disease. This sequence represents the murine NM23A protein described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
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J, Zhang J,
Goodrich R;
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2000US-00598075.
2000US-00620325.
2000US-00654936.
2000US-00663561.
2000US-00693325.
2000US-00693325.
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N-PSDB; AAK52117.
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                                                                                                                                                                                                                                                                                                           Sequence 152 AA;
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27-APR-2000;
20-JUN-2000;
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01-SEP-2000;
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Ma Y, Zhao
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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Pred. No. 1.1e-81
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N-PSDB; AAS61861.
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21-JUN-2000;
01-SEP-2000;
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19-DEC-2000;
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The invention relates to novel isolated lung small cell cancer antigen polynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample from the patient is contacted with (III), detecting the amount of polynucleotide hybridised to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient.

(I), (II) or antigen-presenting cells expressing (II) is useful for atimulating and/or expanding T cells with one of the components under conditions to permit the stimulation and/or expansion of the cells. A conditions to permit the stimulation and/or expansion of the cells. A conditions to patient. An isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of a cancer especially cremoving tumour cells from the biological sample and for inhibiting the development of cancer in a patient. And isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of cancer in a patient. Add(9407-AAU(9431 represent novel human lung small cell cancer antigen amino acid sequences of the
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          sotide and polypeptides useful in therapy and especially lung cancer.
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isease; liver cirrhosis; liver cancer; cytosta
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ed. No. 1.1e-81;
Mismatches 10
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Pred. No.
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gastrointestinal disease; liver
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illarity 91.5%;
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              Lung tumor
diagnosis c
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                                                                        The invention relates to novel biomarkers for liver diseases. The invention also relates to the use of an autoantigen screening method to identify biomarkers that can be used in detecting liver diseases such as liver cirrhosis and liver cancer. The present sequence is the human NM23 protein. This sequence is the autoantigen identified from cell lines using sera of patients with liver cirrhosis and liver cancer.
                                                                                                                                                                                                                              62
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                   sequences, useful r liver cancer.
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3; neoplasm; prognosis; tumor
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                    New biomarker for liver diseases comprising specific s
for developing kits for diagnosing liver cirrhosis or
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The present invention provides a method for analyzing differential protein expression associated with histopathological features of breast disease, in particular breast tumors, e.g. breast carcinomas, comprising detecting the overexpression or underexpression of a pool of proteins in breast tissues or cells. The pool comprises all or part of a protein set comprising: afadin, aurora A, alpha-catenin, beta-catenin, BCL2, cyclin C, cyclin E, cytokeratin S, all B. B. Cadherin, BGRR, ERBB2, ERBB3, ERBB3, ERBB3, ERBB3, estrogen receptor, FGRR1, FHTT, GARC3, cytokeratin G, cytokeratin B, angl, aurora B, BCRP1, cathepsin D, CD10, CD44, CK14, cox2, fibroblast growth factor 2 (FGF2), GATA4, hifla, matrix Gers, posterin, PLAU, S100, SCRIBBEB, smooth muscle actin, thrombospondin (THBS) 1, tissue-inhibitors of matrix metalloprotease (MMP) 9, MTA1, NM23, neuregulins (RRG) 1 alpha, NRG1 beta, p27, parkin, PLAU, S100, SCRIBBEB, smooth muscle actin, thrombospondin (THBS) 1, tissue-inhibitors of matrix metalloprotease 1 (TMMP). The measuring of over- or underexpression of proteins is carried out on tissue microarray, by immunohistochemistry (IHC) technologies. The method may involve comparing expression levels of the protein set in a control sample to levels of equivalent proteins in a tissue sample. The detection may also involve detecting the over- or underexpression of nucleic acids coding for the proteins. Also claimed are a protein library and a nucleic acid library useful for the molecular characterization of histopathological features of breast disease. The method is useful for analyzing differential protein expression associated with breast cancer, predicting claimed associated with breast cancer, predicting a predicting of breast cancer, predicting of breast cancer. Teratment of a patient can be based on the analysis of the protein of a patient can be based on the analysis of the protein of a patient can be besed on the method is a breast cancer.
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The present sequence is the human nm23 protein nm23-H1, the gene for which is found on chromosome 17q21. Its coding sequence was isolated by searching a human fibroblast cDNA library for sequences similar to pnm23-M1. Nm23 proteins are involved in tumour metastasis, and this protein, its gene and antibodies can be used to determine an individual's susceptibility to cancer and the likelihood of tumour metastasis within that individual. This is possible using a number of methods, including Northern blotting, nuclease protection assays, in situ hybridisation, immunohistochemical analysis and solid phase immunoassays
                                                                                                                                                                                                                       useful
                                                                                                                                                                                                                       New nm23 monoclonal antibody which recognizes human nm23 protein, usefu
for detecting tumors which have low levels of nm23 protein and thus an
increased ability to metastasize or be malignant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; malignant potential;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 794; DB 3;
Pred. No. 1.1e-81;
4; Mismatches 10;
         amino
                                                                                                                                       SERVICES
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          "putative first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 AA
                                                                                                                                                               GR;
                                                                                                                                       & HUMAN
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                                                                                                                                                                                                                                                                      Claim 1; Fig 6; 21pp; English.
                                                                                                     89US-00422801
91US-00806932
                                                                              95US-00475684
                                                                                                                                                                                                                                                                                                                                                                                                                                  90.6%;
91.5%;
                                                                                                                                                             King
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAO26422 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein of the nm23-H1
                                                                                                                                       DEPT HEALTH
          /note=
                                                                                                                                                               Steeg PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                 N-PSDB; AAA70316
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 183 AA;
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6423836-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                     18-OCT-1989;
11-DEC-1991;
                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUL-2002
                                                        11-JUL-2000
                                 US6087117-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          150;
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                                                                                                                                                              Liotta LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
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                                                                                                                                       (USSH)
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                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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New human NM23
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                                                                                                                                assessment of
         18-OCT-1989;
11-DEC-1991;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                           Query Match
                                                                     CR,
                                                                                                                                                                                                                                                                                                                    Local
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                                                 (USHE-)
                                                                                                                                                                                                                                                                  tumour
                                                                                                                                                    Claim
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Matches
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AAE2172
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                                                                                                                                                              encoding a
746 base pairs
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                                                                                                                                                                                                                                                                            nm23
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                                                                                                             the
                                                                                                                                                                   The invention relates to an isolated polynucleotide molecule encoding a human nm23 protein comprising nm23-H1 having a sequence of 746 base pai (bp) fully defined in the specification or nm23-H2S having a sequence of 670 bp fully defined in the specification. The polynucleotide molecule the invention is useful as a diagnostic tool for detecting and/or determining RNA or DNA which can be employed to detect mRNA expression cancer cells to aid in predicting the malignant potential of a human tumour. The DNA and the antibodies may also be used to detect abnormalities of DNAs in normal or cancer cells to aid in predicting the genetic predisposition for developing cancer. The human nm23 protein cabe employed to produce nm23 antibodies. This sequence represents the nm-H1 protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                 IRGDE
                                                                                                                                                                                                                                                                                                                                                                                         SEDLL
                                                                                                                                                                                                                                                                                                                                                                                                               IRGDE
                                                                                                                                                                                                                                                                                                                                                                       SEDLL
                                                                                                              ting
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                            New DNA molecule encoding a human nm23 protein useful for predicamalignant potential of a tumor and the genetic predisposition for developing cancer, comprises nm23-H1 and nm23-H2s genes.
                                                                                                                                                                                                                                                                                                                                                                      OPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQA
                                                                                                                                                                                                                                                                                                                                                                                   KEHYVDLKDRPFFAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour;
                                                                                                                                                                                                                                                                                                                                                                                                              KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGT
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                               Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metastatic potential; t
familial breast cancer.
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE
                                                                                                                                                                                                                                                                                                                                            31,
10;
                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                              Score 794; DB 5;
Pred. No. 1.1e-81
1; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NM23-H1 encoded from full length cDNA
                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33. .184
/label= Mature NM23-H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NM23-H1; NM23-H2S; aggressiveness; cancer susceptibility; early-onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; protein; 184
                                                            Liotta LA;
                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                     21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00335948
 91US-00806932
                     89US-00422801
                                                                                                                                                                                                                                                                                                                                90.6%;
91.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                               WPI; 2002-705184/76
N-PSDB; AAL53614.
                                                            Steeg PS,
                                                                                                                                                                                                                                                                                                                                         Local Similarity
ses 150; Conser
                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                            Sequence 184 AA;
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11-DEC-1991;
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                    18-OCT-1989;
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                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                            King CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                                                                                                                                                                                                                                                    Matches
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The sequences given in AAG79335-38 show the related human proteins NM23-H1 had H2S. These proteins are products of different genes, with NM23-H1 being localised to chromosome 17. These proteins are used to predict aggressiveness (metastatic potential) of human tumours and in genetic tests for cancer susceptibility, diagnosis and prognosis, also for selection of treatment, e.g. susceptibility to early-onset familial breast cancer. Gene nm23 may contribute to tumourigenicity and alteration in its regulation may be an early stage in the metastatic cascade.
                                                                                                                                                                                                                                       and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; kinase; enzyme; PKIN-19 protein; immune system disorder; anaemia; acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease; asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease; AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder; Down's syndrome; gene therapy; protein therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                     cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                protein, useful for diagnosis and prognosis of aggressiveness and susceptibility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16. .177
/label= Human_mature_PKIN-19_protein
120. .168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1e-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                    HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SO.
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/label= Signal_peptide
16. .177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 177
                                                                                                                              Liotta LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ;
89US-00422801.
91US-00806932.
95US-00475684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.6%;
ilarity 91.5%;
Conservative
                                                                                                                                                                                                                                                                                                     23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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                                                                                     SEC
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                                                                                                                                                                                                                                                                                                    23-24;
                                                                                                                              Steeg PS,
                                                                                                                                                                        2002-121137/16
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PA XX
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PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              sarcoma),
                                                                                                                                                                                                                                                                                                                  (e.g.
1 leukemia
                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to human kinases (PKIN) and polynucleotides encoding such proteins. PKIN sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of PKIN, particularly immune system disorders (e.g. acquired immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease, anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-Tooth disease or seizures), cell proliferative disorders (e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tooth disease or seizures), cell proliferative disorders (e.g. cancers such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma, and developmental disorders (e.g. Down's syndrome). They are also used gene therapy and protein therapy. The present sequence is human PKIN-19
                                                                                                                                                                                                                                                                                                        immune
                                                                                                                                                                                       O, Nguyen DB, Walia NK, Hafalia AJA, Yao MG, Gandhi AR; an R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM; M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT; Y, Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG; J, Warren BA, Kearney L, Policky JL, Thangavelu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGDFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                    New human kinases, useful for diagnosing, treating or preventing system disorders (e.g. Crohn's disease), neurological disorders epilepsy), or cell proliferative disorders (e.g. cancers such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQAS
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Pred. No. 1.8e-79;
1; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4,
                                                                                                                                                                                                                                                                                                                                                            74; Page 183-184; 218pp;
                                                                          2000US-0229873P.
2000US-0231357P.
2000US-0232654P.
2000US-0234902P.
2000US-0236499P.
2000US-0238389P.
                                                       2001WO-US027219
                                                                                                                                            2000US-0240542P
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                                                                                                                                                                    INCYTE GENOMICS INC
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N-PSDB; AAD34316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 AA;
            WO200218557-A2
                                                                                    08-SEP-2000;
14-SEP-2000;
22-SEP-2000;
29-SEP-2000;
06-OCT-2000;
13-OCT-2000;
                                                       31-AUG-2001;
                                                                                                                                                                                                              Thornco-Azimzai Y,
                                                                                                                                                                                                                                                                                                                                      or lymphoma)
                                                                                                                                                                                                            Thornton M,
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                                 07-MAR-2002
                                                                                                                                                                                                                                               Burford N;
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                                                                                                                                                                    (INCX-)
                                                                                                                                                                                        Bandman
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Matches
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This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer. Or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection brostatic tissue. Screening for inhibitors of the sequences or detection cubstances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonuclectides, with tumour cells. Inhibitors can be chosen from antisense oligonuclectides, ending the below 5000, preferably 300, that binds to the polypeptide; weight below 5000, preferably humanised or human; an anti-idotype, non-human conjugated below 5000, preferably humanised or human; an anti-idotype, non-human conclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or andocional) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or cancer by differential expression analysis, using by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected sequentially with anti-human CD4 murine monoclonal antibodies; by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of sequentially with anti-human CD4 murine monoclonal antibodies; conterpationed with hemalum (blue). Malignant cells stained sequence and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the incorporation and polympetide sequences used in the metastases the prostatic ander pariety of the prostatic ander pariety of the prost
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:ke S;
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Pred. No. 2.2e-78;
; Mismatches 6;
                                                       atic; diagnosis; prostatic cancer; expression analysis.
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prostatic carcinoma derived DNA SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               German.
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2003DE-01022134
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ROSENTHAL A.
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                                                        human; cytostatic;
differential expres
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                                                                                                                                                                                                          WO2004076614-A2
                                                                                                                                                                                                                                                                                                                              22-FEB-2004;
                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-2003;
14-MAY-2003;
                                                                                                                                                   Homo sapiens
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Xinzhong L,
                                                                                                                                                                                                                                                                      10-SEP-2004
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Best Local S
Matches 144
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(PILA/)
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(ROSE/)
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This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer. Cor the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are celected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays. between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from
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non-human
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                           LKDRP
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TMANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVD
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nann H, Roepcke
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diagnosis, treatment and in screening for specific bi
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                                                                                                                                                                                                                                                                                       236
                                                                                                                                                                                                                                                                                      Human prostatic carcinoma derived protein SEQ ID
                                                                                                                                                                                                                                                                                                                   human; cytostatic; diagnosis; prostatic cancer; differential expression analysis.
                                                                                      166
                                                                                                     SDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 153
                                                                                      SDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE
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                                                                                                                                                                                              ADR66040 standard; protein; 153
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2003DE-01022134
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Staub E;
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PILARSKY C
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14-MAY-2003;
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Xinzhong L,
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(ROSE/)
(HERM/)
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prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polynucleotide and polypeptide sequences used in the method of the
                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                            73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   paralysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleoside diphosphate kinase 19.47 (ABB99909) and nucleic acids encoding it (ABQ77987). The protein has a molecular weight of 19.47 kD. The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the protein, gene and antagonist in therapeutic applications Nucleoside diphosphate kinase 19.47 can be used in the treatment of a variety of diseases such as tumours, embryonic development disorders and
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                                                                                                                                                                                      Length 153;
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                                                                                                                                                                       Score 764; DB 8; Le
Pred. No. 2.2e-78;
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                                                                                                                                                                                                                                                                                                                                                       SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide diphosphate kinase 19.47
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cancer;
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                                                                                                                                                                                      87.2%;
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gene therapy; tumour; o
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B; ABQ77987.
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cytostatic;
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                                                                                                                                                                                                                144;
                                                                                                                                invention
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carcinoma; human; neuroblastoma.

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The present sequence represents human nm23-H1 protein. The specification describes a method for the diagnosis of metastatic potential of a carcinoma in a patient. The method comprises obtaining a sample of chromosomal DNA from the tumour of the subject, and analysing the sample of chromosomal DNA for the presence or absence of a human nm23-H1 allele. The absence of a human nm23-H1 allele indicates metastatic potential. The subject has previously had or currently has breast carcinoma, non-small cell lung carcinoma or kidney carcinoma. The metastatic potential is due to allelic deletions in the human nm23 gene, nm23-H1. The method can also be used for the diagnosis of colorectal carcinoma or neuroblastoma in patients who have had or currently have such carcinomas
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               potential; carcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosis of metastatic potential of carcinoma - chromosomal DNA sample from the patient's tumour of human nm23-H1 allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 2;
8.3e-78;
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                                                166
                                                                                                                                                                                                                           metastatic
colorectal
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                                                            DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE
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                                                                                                                                                                                                                           diagnosis; deletion;
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89US-00422801.
90US-00528713.
91US-00775081.
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N-PSDB; AAV38413.
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143; Conser
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1 allele;
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                                                                                                                                                                                                      nm23-H1
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18-OCT-1989;
24-MAY-1990;
11-OCT-1991;
02-FEB-1994;
                                                                                                                                                                                                                                                              sapiens
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nm23-H1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding this human nm23 protein is useful for detecting mRNA expression in cancer cells and for helping predict the malignant potential of a human tumour. This nm23 protein is useful for raising antibodies for detecting tumours having low levels of nm23 protein and thus an increased ability to undergo metastasis or be malignant. See ala AAQ11721
                                                                                                                         EDLLK
                                                                                                                                                        RGDFC
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   diphosphat
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predict metastasis, malignant potential and aggression of human
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                                                             Length 177
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                                                                                    Indels
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   nucleoside
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; Pred. No. 8.3e-78;
                                                  Score 761.5; DB 5;
Pred. No. 5.3e-78;
    represents
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    sednence
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94.1%;
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                                     177 AA;
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  The
                                                                                                                                                                                                                                                                                                                                                                               nm23;
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paralysis.
19.47
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Gaps

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Length 152;

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Pred. No. 8.3e-78;
; Mismatches
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                        166
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                       DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE
                                                                                                                                                                                                      NM23-H1; NM23-H2S; aggressiveness; cancer susceptibility; early-onset
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                                                                                                          standard, protein;
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                                                                                                                                                                              Mature human NM23-H1
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N-PSDB; AAI72921.
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nes 143; Conser
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11-DEC-1991;
07-JUN-1995;
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US-10-074-694-3 876 Title: Perfect score:

.....weqpeelveykscaqnwiye QSQPAVKPCHLKGTMANSER Sequence:

0.5 Gapext -BLOSUM62 Gapop 10.0 Scoring table:

96216763 residues 283416 seqs, Searched:

hits satisfying chosen parameters of Total number

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PIR 80:* Database

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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 A46557 nucleoside-diphosphate kinase (EC 2.7.4.6) - mouse (fragment) N;Alternate names: differentiation-inhibiting factor; tumor metastasis inhibitor NM23 C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 03-Mar-1994 #sequence revision 03-Mar-1994 #text_change 05-Oct-2004 C;Accession: A46557; B33386; T52807; JN0281 R;Steeg, P.S.; Bevilacqua, G.; Kopper, L.; Thorgeirsson, U.P.; Talmadge, J.E.; Liotta, L. J. Natl. Cancer Inst. 80, 200-204, 1988 A;Title: Evidence for a novel gene associated with low tumor metastatic potential. A;Reference number: A46557; MUID:88155671; PMID:3346912 A;Accession: A46557 A;Accession: A46557 A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-166 <ste> A;Residues: 1-166 <ste> A;Cross-references: UNIPROT:P15532; UNIPARC:UP1000016CF64; GB:M35970; NID:g200066; PIDN:A</ste></ste>	A; Note: the authors translated the codon TGG for residue 163 as Tyr R; Rosengard, A.M.; Krutzsch, H.C.; Shearn, A.; Biggs, J.R.; Barker, E.; Margulies, I.M.K. Nature 342, 177-180, 1989 A; Title: Reduced Nm23/Awd protein in tumour metastasis and aberrant Drosophila developmer A; Reference number: A33386; MUID: 90044071; PMID: 2509941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: sequence extracted from NCBI backbone (NCBIP:124170)
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; pl
F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status predic
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A; Cross-references: UNIPROT: P15531; UNIPARC: UPI0000112099; GB:X75598
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A;Experimental source: skeletal muscle
A;Note: sequence extracted from NCBI backbone (NCBIP:124170)
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Pred. No. 6.4e-67;
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A;Residues: 1-152
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R;Dooley, S.; Seib, T.; Engel, M.; Theisinger, B.; Janz, H.; Piontek, Hun. Genet. 93, 63-66, 1994
A;Title: Isolation and Characterization of the human genomic locus cod A;Reference number: 845376; MUID:94095204; PMID:8270257
A;Accession: 845376; MUID:94095204; PMID:8270257
A;Accession: 845376; MUID:94095204; PMID:8270257
A;Accession: 845376; MUID:94095204; PMID:8270257
A;Accession: 845376; MUID:94095204; PMID:870257
A;Cross-references: UNIPARC:UPIO000112099; EMBL:X75599; NID:9468541; PR;Ailles, AM.; Presecan, E.; Vonnice, A.; Lascu, I.
A;Title: Nuclosoide diphosphate kinase from human erythrocytes. Struct A;Reference number: A39938; MUID:91224972; PMID:1851158
A;Accession: A39938
A;Molecule type: protein
A;Reference number: A39938; MUID:91224972; PMID:1851158
A;Accession: A39938
A;Molecule type: protein
A;Reference number: A43931; MUID:91277302; PMID:2056128
A;Accession: A49931
A;Title: High levels of p19/mm23 protein in neuroblastoma are associat A;Accession: A49331
A;Molecule type: protein
A;Accession: A49331
A;Molecule type: protein
A;Accession: A49331
A;Molecule type: protein
A;Accession: A49331
A;Molecule type: protein
A;Accession: A59838
A;Molecule type: protein
A;Accession: A59838
A;Molecule type: protein
A;Accession: A56882; MUID:93153759; PMID:7916650
A;Accession: A56882; MUID:93153759; PMID:791650
A;Accession: A7102; L14072
A;Antrons: A111777
A;Antrons: A1117
A;Cross-references: UNIPARC:UPIO00017564
A;Accession: A1104
A;Cross-references: UNIPARC:UPIO00017640
A;Accession: A56882; 
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Pred. No. 5.2e-65;
; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSVKSAEKEISLWFOPEELVEYKSCAONWIYE 166
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                                                                        nucleoside
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C; Species: Mus musculus (house mouse)
C; Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-C; Accession: S29241
R; Urano, T.; Takamiya, K.; Furukawa, K.; Shiku, H.
FEBS Lett. 309, 358-362, 1992
A; Title: Molecular cloning and functional expression of the second mouse A; Title: Molecular cloning and functional expression of the second mouse A; Reference number: S29241; MUID:92387389; PMID:1325378
A; Reference number: S29241; MUID:92387389; PMID:1325378
A; Residues: 1-152 <URA>
A; Residues: 1-152 <URA>
A; Cross-references: UNIPROT: Q01768; UNIPARC: UPI0000003EFD; EMBL:X68193; C; Superfamily: nucleoside diphosphate kinase C; Superfamily: nucleoside diphosphohistidine; phosphoprotein; phosphoprotein; F; 118/Active site: His (phosphohistidine intermediate) #status predicted
A; Cross-references: UNIPARC: UPI000012FE93; GB:M55331; GB:J05588; NID:g2(R; Ishikawa, N.; Shimada, N.; Munakata, Y.; Watanabe, K.; Kimura, N. J. Biol. Chem. 267, 14366-14372, 1992
A; Title: Isolation and characterization of a gene encoding rat nucleosic A; Title: Isolation and characterization of a gene encoding rat nucleosic A; Reference number: A42967; MUID:92332552; PMID:1321145
A; Reference number: A42967; MUID:92332552; PMID:1321145
A; Reference number: A42967; MUID:92332552; PMID:1321145
A; Residues: 1-152 < ISH>
A; Molecule type: DNA
A; Residues: 1-152 < ISH>
A; Residues: 1-152 < ISH>
A; Note: sequence extracted from NCBI backbone (NCBIN:108562, NCBIP:108562; Note: sequence extracted diphosphate kinase
C; Superfamily: nucleoside diphosphate kinase
C; Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphohistidine intermediate) #status predicted
F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate)
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Pred. No. 2.7e-61;
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Pred. No. 3.3e
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E.H.; Berberich, S.J.; Flint, S.J.; Ferrone, C.A.
51, 478-480, 1993
Human c-myc transcription factor PuF identified as nm23-H2ce number: I59581; MUID:93324921; PMID:8392752
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C; Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein;
F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status pred
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C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change C;Accession: A41849; A38369; A42967
R;Hemmerich, S.; Yarden, Y.; Pecht, I.
Biochemistry 31, 4574-4579, 1992
A;Title: A cromoglycate binding protein from rat mast cells of a A;Reference number: A41849; MUID:92256389; PMID:1316151
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                                                                                                                                              Gilles, A.M.; Presecan, E.; Vonica, A.; Lascu, I.
Biol. Chem. 266, 8784-8789, 1991
Title: Nucleoside diphosphate kinase from human erythrocytes
Reference number: A39838; MUID:91224972; PMID:1851158
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PMID:2168422
               A49798; MUID:91105674; PMID:1988104
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A; Residues: 1-152 < HEM>
A; Residues: 1-152 < HEM>
A; Cross-references: UNIPROT: P19804; UNIPARC: UP100
R; Kimura, N.; Shimada, N.; Nomura, K.; Watanabe,
J. Biol. Chem. 265, 15744-15749, 1990
A; Title: Isolation and characterization of a CDN/
A; Reference number: A38369; MUID: 90368787; PMID: A; Accession: A38369
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                                                                                                                      Cross-references: UNIPROT: P22392; UNIPAIGILLES, A.M.; Presecan, E.; Vonica, A.; Biol. Chem. 266, 8784-8789, 1991
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11 Similarity 90.1%;
137; Conservative
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C;Superfamily: nucleoside d
        A; Reference number: A49798
A; Accession: A49798
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-152 <STA>
A; Cross-references: UNIPRO
R; Gilles, A.M.; Presecan,
J. Biol. Chem. 266, 8784-8
A; Title: Nucleoside diphos
A; Reference number: A39838
A; Accession: B39838
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-152 <GIL>
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A;Molecule type: mRNA
A;Residues: 1-152 <KI
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A; Accession: I59581
A; Status: translated
A; Molecule type: mRNA
A; Residues: 1-152 < RE
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A; Cross-references: UR; Postel, E.H.; Berbe
Science 261, 478-480,
A; Title: Human c-myc
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UNIPARC:UPI000012FE9C; GB:U18906; NID:g619942; PIDN:7 enzyme in the synthesis of nucleotide triphosphates cGTP-binding proteins and a role in signal transductic
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C;Species: Brugia malayi
C;Species: Brugia malayi
C;Species: Brugia malayi
C;Date: 08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-;
C;Date: 08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-;
C;Accession: JC4359
R;Ghosh, I.; Raghavan, N.; FitzGerald, P.C.; Scott, A.L.
Gene 164, 261-266, 1995
A;Title: Nucleoside diphosphate kinase from the parasitic nematode Brugi
A;Reference number: JC4359; MUID: 96069592; PMID: 7590340
A;Reference number: JC4359; MUID: 96069592; PMID: 7590340
A;Residues: J-153 <GHO>
A;Residues: I-153 <GHO>
A;Residues: I-153 <GHO>
A;Cross-references: UNIPROT: P48817; UNIPARC: UPIO0012FE9C; GB: U18906; NI
C;Comment: This enzyme is a pivotal enzyme in the synthesis of nucleotic de triphosphates, supplying GTP for GTP-binding proteins and a role in & C;Genetics:
A;Gene: ndk
C;Genetics:
A;Gene: ndk
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phos F;13-17/Region: ATP binding #status predicted
F;106/Active site: Arg #status predicted
F;106/Active site: His (phosphohistidine intermediate) #status predicted
F;119/Active site: His (phosphohistidine intermediate)
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Pred. No. 3.3e-42;
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Pred. No. 4.6e-43;
3; Mismatches 29;
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                                                                                                                                                                                      hypothetical protein F25H2.5 - Caenorhabd C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15 C; Accession: T21354  
R; Wilkinson, J. submitted to the EMBL Data Library, Septer A; Reference number: Z19411  
A; Reference number: Z19411  
A; Reference number: Z19411  
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A; Reference number: Z19411  
A; Residues: 1-153 < WIL> A; Residues: 1-153 < WIL> A; Residues: CESP:F25H2.5  
A; Genetics: A; Genetics: A; Genetics: A; Map position: 1  
A; Introns: 18/2; 49/3  
C; Superfamily: nucleoside diphosphate kin
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C; Species: Drosophila melanogaster
C; Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-:
C; Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-:
C; Accession: S01908
R; Biggs, J.; Tripoulas, N.; Hersperger, E.; Dearolf, C.; Shearn, A.
Genes Dev. 2, 1333-1343, 1988
A; Title: Analysis of the lethal interaction between the prune and kille:
A; Reference number: S01908; MUID:89079007; PMID:2849580
A; Accession: S01908
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: UNIPROT:P08879; UNIPARC:UPI0000011C4; EMBL:X13107;
C; Genetics:
A; Gene: awd
A; Cross-references: FlyBase:FBgn0000150
A; Map position: 3 100C-D
C; Superfamily: nucleoside diphosphate kinase
C; Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotive site: His (phosphohistidine intermediate) #status predicted
F; 119/Active site: His (phosphohistidine intermediate)
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;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein;
;32-36/Region: ATP binding #status predicted
;134/Active site: His (phosphohistidine intermediate) #status pred
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C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_chang C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_chang C; Accession: 139074
R; Venturelli, D.D.; Martinez, R.R.; Calabretta, B.B. Proc. Natl. Acad. Sci. U.S.A. 92, 7435-7439, 1995
A; Title: Overexpression of DR-nm23, a protein encoded by a mem A; Reference number: 139074; MUID:95365382; PMID:7638209
A; Reference number: 139074; MUID:95365382; PMID:7638209
A; Reference number: 139074; MUID:95365382; PMID:7638209
A; Reference number: 139074; MUID:95365382; PMID:7638209
A; Reference number: 139074; MUID:95365382; PMID:7638209
A; Residues: 1-168 < RES>
A; Residues: 1-168 < RES>
A; Residues: 1-168 < RES>
A; Cross-references: UNIPROT:Q13232; UNIPARC:UPIO00149FCF; EMB C; Gene: GDB:NME3; DR-nm23
A; Cross-references: GDB:5215169; OMIM:601817
A; Map position: 16q13-16q13
C; Superfamily: nucleoside diphosphate kinase C; Keywords: ATP binding #status predicted F; 134/Active site: His (phosphohistidine intermediate) #status F: 134/Active site: His (phosphohistidine intermediate)
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Pred. No. 8.1e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 611; DB 2; 1
Pred. No. 6.5e-51;
5; Mismatches 20;
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ilarity 66.2%;
Conservative 3:
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11 Similarity 76.2%;
115; Conservative 1
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phosphoprotein; phosphotransferase;
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C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C; Accession: T08909
R; Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, B; Bevan, M.; Zimmermann, W.; Grueneisen, May 1999
A; Reference number: Z16518
A; Reference number: Z16518
A; Reference number: Z16518
A; Molecule type: DNA
A; Residues: 1-237 <BEV>
A; Cross-references: UNIPROT: Q8LAH8; UNIPARC: UPI00000ABF3A; EMBL: AL078468; GSPDB
A; Experimental source: cultivar Columbia; BAC clone T32A16
C; Genetics:
A; Gene: ATSP: T32A16.70
A; Map position: 4
A; Introns: 28/1; 74/1; 86/3; 103/3; 159/3; 197/2
C; Superfamily: nucleoside diphosphate kinase
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A; Experimental source: cultivar Columbia; BAC clone F25124
C; Genetics:
A; Gene: ATSP:F8M12.12; ATSP:F25124.220; ndpk3
A; Map position: 4
A; Introns: 28/1; 75/1; 87/3; 104/3; 160/3; 198/2
C; Superfamily: nucleoside diphosphate kinase
C; Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosp.
C; Keywords: ATP binding #status predicted
F; 99-103/Region: ATP binding #status predicted
F; 123/Active site: Lys #status predicted
F; 202/Active site: His (phosphohistidine intermediate) #status predicted
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31;
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32;
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ed. No. 2.4e-41;
Mismatches 32
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Pred. No. 1.9e-41
27; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235
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Best Local Similarity 62.7%;
Matches 94; Conservative 24
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NiAlternate names: protein F25124.220; protein F8M12.12
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-20
C; Accession: T01877; T04296
R; Madsen, C.; Graves, T.; Cotton, M.; Modde, T.
Submitted to the EMBL Data Library, July 1998
A; Description: The sequence of A. thaliana F8M12.
A; Reference number: Z14450
A; Accession: T01877
A; Reference number: Z14450
A; Accession: T01877
A; Reference Lype: DNA
A; Residues: 1-238 <AMAD>
A; Residues: 1-238 <AMAD>
A; Experimental source: cultivar Columbia
R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft submitted to the Protein Sequence Database, March 1999
A; Reference number: Z15261
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A; Residues: 1-149 <F12>
A; Cross-references: UNIPROT: P47922; UNIPARC: UPI000012FE7F; EMBL: X7138
A; Note: submitted to the EMBL Data Library, April 1993
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C; Species: Pisum sativum (garden pea)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-c; Accession: S46513; S33170
R; Finan, P.M.; White, I.R.; Redpath, S.H.; Findlay, J.B.C.; Millner, Plant Mol. Biol. 25, 59-67, 1994
A; Title: Molecular cloning, sequence determination and heterologous A; Reference number: S46513; MUID:94272014; PMID:8003697
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A;Residues: 1-238 <BEV>
A;Cross-references: UNIPARC:UPI000012FE87; EMBL:AL049525;
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Pred. No. 9.7e-42;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-148 cGRA>
A; Cross-references: UNIPROT: Q96559; UNIPARC: UPI000012FEAB; EMBL: U72142; NID: g1619957; PI
C; Function:
C; Function: catalyzes transfer of the gamma-phosphate group from ATP to nucleoside di
C; Function:
A; Description: catalyzes transfer of the gamma-phosphate group from ATP to nucleoside di
c; Superfaming: UTP for polysaccharide synthesis, CTP for lipid synthesis and GTP for pro
c; Superfamily: nucleoside diphosphate kinase
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C; Superfamily: phosphotransferase; pyrimidin
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Pred. No. 2.3e-41;
8; Mismatches 32;
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Search completed: December 16, 2005, 16:39:05 Job time: 25.5346 secs

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using sw model protein search, OM protein

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US-10-074-694-5 803 Perfect score:

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SUMMARIES

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ALIGNMENTS

nm23-H2

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A; Recession: A49798; MUID:9120497; PMID:19864; GB:X58965; NID:935069; PIDN:
A; Recession: A49798; MUID:91224972; PMID:1851158
A; Reference number: A39818; MUID:91224972; PMID:1851158
A; Researce number: A39818; MUID:9324921; PMID:8392752
A; Researce number: B5881; MUID:93324921; PMID:8392752
A; Researce number: 159581; MUID:93324921; PMID:93494475; PIDN:AAA60228.1; PID
A; Researce number: 159581; MUID:93324921; PMID:8392752
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152; Length Score 803; DB 2; Pred. No. 1.8e-71; ; Mismatches 0; 0; Query Match Best Local Similarity 100.0%; Matches 152; Conservative 0

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Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein;
15-19/Region: ATP binding #status predicted
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C.Date: 28-Jun-1991 #sequence revision 28-Jun-1991 #text_change C.Date: 28-Jun-1991 #sequence revision 28-Jun-1991 #text_change C.Date: 28-Jun-1991 #sequence revision 28-Jun-1991 #text_change C.Date: 28-Jun-1991 #sequence revision 28-Jun-1991 #text_change R.Hemmerich, S: Yarden, V: Pecht, I.
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A.Accession: A1849
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A.Accession: A1849; MUID:92256389; PMID:1316151
B.A.Accession: A1840; MUID:9036879; PMID:168422
A.Accession: A38369
A.Status preliminary
A.Molecule type: MRM
A.Residues: 1.152 KIM>
A.Accession: A38369; MUID:90368787; PMID:2168422
A.Accession: A38369
A.Status preliminary
A.Molecule type: MRM
A.Residues: 1.152 KIM>
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B.Ishikawa, N.; Shimada, N.; Munakata, Y.; Matanabe, K.; Kimura, U. Biol. Chem. 267, 14366-1472, 1992
A.Accession: A42967
A.Ac
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nucleoside-diphosphate kinase (EC 2.7.4.6) B - mouse
C; Species: Mus musculus (house mouse)
C; Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_cha
C; Accession: S29241
R; Urano, T.; Takamiya, K.; Furukawa, K.; Shiku, H.
FEBS Lett. 309, 358-362, 1992
A; Title: Molecular cloning and functional expression of the
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A; Reference number: S29241; MUID: 92387389; PMID: 1325378
A; Accession: S29241
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-152 < URA>
A; Residues: 1-152 < URA>
A; Cross-references: UNIPROT: Q01768; UNIPARC: UPI0000003EFD; EMBL: X68193; NID: g53353; PIDIC; Superfamily: nucleoside diphosphate kinase
C; Superfamily: nucleoside diphosphohistidine; phosphoprotein; phosphotransferase; C; Keywords: ATP binding #status predicted
F; 15-19/Region: ATP binding #status predicted
F; 118/Active site: His (phosphohistidine intermediate) #status predicted
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A450Secies: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C; Accession: A45208
R; Shimada, N.; Ishikawa, N.; Munakata, Y.; Toda, T.; Watanabe, K.; Kimura, N.
J; Biol. Chem. 268, 2583-2589, 1993
A; Title: A second form (beta isoform) of nucleoside diphosphate kinase from rat. Isola
A; Reference number: A45208
A; Status: preliminary
A; Residues: 1-152 <SHI>
A; Residues: 1-152 <SHI>
A; Residues: 1-152 <SHI>
A; Cross-references: UNIPROT:Q05982; UNIPARC:UPI000012FE91; GB:D13374; NID:g286231; PID
A; Cross-reference extracted from NCBI backbone (NCBIP:124170)
C; Superfamily: nucleoside diphosphate kinase
C; Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase
C; Keywords: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status predicted
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A46557
nucleoside-diphosphate kinase (EC 2.7.4.6) - mouse (fragment)
N;Alternate names: differentiation-inhibiting factor; tumor metastasis inhibitor C;Species: Mus musculus (house mouse)
C;Species: Mar-1994 #sequence revision 03-Mar-1994 #text_change 05-Oct-2004
C;Accession: A46557; B33386; T52807; JN0281
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Pred. No. 1.7e-64
10; Mismatches
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ilarity 98.0%;
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Best Local Similarity 90.1%;
Matches 137; Conservative 1
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G.M.; Reynol

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A,Reference number: A33366; MUID:90044071; PMID:2509941
A,Accession: A33366 with conceptual translation
A,Status: not compared with conceptual translation
A,Ratus: not compared with conceptual translation
A,Ratus: not compared with conceptual translation
A,Residues: 1.122 cRGS.
A,Foctos: This color, 6.3 cRib. 6.1. 1982, M.; Thistinger, B.; Janz, H.; Piontek, K.; Zang, K.D.; M.
A,Residues: 1.122 cRGS.
A,Reference number: 248376; MUID:94095204; PMID:8270257
A,Reference number: 248376; MUID:910309; PMBL:X75598; NID:9468541; FIDN:CAA51270.1; PI
R,Gilles, A.M.; Prescon, E.; Vonnie, A.; Lascu, I.
A,Reference number: 35838; MUID:9124972; PMID:1851158
A,Reference number: 35838; MUID:91224972; PMID:1851158
A,Reference number: 35838; MUID:91224972; PMID:1851158
A,Reference number: 38838; MUID:9124972; PMID:1851158
A,Reference number: 38838; MUID:9124972; PMID:1851158
A,Reference number: 38838; MUID:9124972; PMID:1956128
A,Reference number: 38838; MUID:9124972; PMID:1956128
A,Reference number: 38838; MUID:913199; PMID:916550
A,Reference number: 38838; MUID:913199; PMID:91650
A,Reference number: 36882; MUID:913199; PMID:91650
A,Reference number: 36882; MUID:913199; PMID:91650
A,Reference number: 458882; MUID:913199; PMID:91660
A,Reference number: 458882; MUID:913199; PMID:91660
A,Reference number: 458882; MUID:913199; PMID:91660
A,Reference number: 458882; MUID:919180ACC
C,Superfamil
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S01908
nucleoside-diphosphate kinase (EC 2.7.4.6) - fruit fly (C
N;Alternate names: K-pn protein; killer-of-prune protein
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site: His (phosphohistidine intermediate) #status predicted
      R;Steeg, P.S.; Bevilacqua, G.; Kopper, L.; Thorgeirsson, U.P.; Talmadge, J. Mall. Cancer Inst. 80, 200-204, 1988

A,Title: Evidence for a novel gene associated with low tumor metastatic A,Title: Evidence for a novel gene associated with low tumor metastatic A,Tetle: Evidence for a novel gene associated with low tumor metastatic A,Accession. A46557; MUID:88155671; PMID:3346912

A,Accession. A46557; MUID:88155671; PMID:3346912

A,Accession. AAM; KRUATZEN, H.C.; Shearn, A. Biggs, JR.; Barker, B.; ARCHECE 4AAM; ARCHIVER, H.C.; Shearn, A. Biggs, JR.; Barker, B.; ARCHECE 4AA, A. KRUATZEN, H.C.; Shearn, A. Biggs, JR.; Barker, B.; Natue: 342, 177-1800, 1989

A,Title: Reduced Nus21Awd protein in tumour metastasis and aberrant Droi A,Recession. B33386; MUID:90044071; PMID:2509941

A,Accession. B33386; MUID:90044071; PMID:2509941

A,Accession. B33386; MUID:90044071; PMID:2509941

A,Accession. B33386; MUID:90044071; PMID:2509941

A,Accession. B33386; MUID:91034089; MA.; Margulies, I.M.; Lical and a state and a 
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Pred. No. 3.7e-64;
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720; DB 1;
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(Drosophila melanogaster)

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RESULT 9

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Indoeside-diphosphate kinase (EC 2.7.4.6) DR-nm23 - human
N;Alternate names: DR-nm23 protein; non-metastatic cell-expressed protein 3
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C;Accession: 139074
R;Venturelli, D.D.; Martinez, R.R.; Calabretta, B.B.
Proc. Natl. Acad. Sci. U.S.A. 92, 7435-7439, 1995
A;Title: Overexpression of DR-nm23, a protein encoded by a member of the nm23 gene famil A;Reference number: 139074; MUID:95365382; PMID:7638209
A;Accession: 139074
A;Reference number: 139074; MUID:95365382; PMID:7638209
A;Accession: 139074
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-168 <-RES.
A;Cross-references: UNIPROT:Q13232; UNIPARC:UP10000149FCF; EMBL:U29656; NID:g1051255; PI)
C;Genetics:
A;Gene: GDB:NME3; DR-nm23
A;Cross-references: GDB:5215169; OMIM:601817
A;Map position: 16q13-16q13
C;Superfamily: nucleoside diphosphate kinase
C;Superfamily: nucl
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C;Species: Brugia malayi
C;Species: Brugia malayi
C;Species: Brugia malayi
C;Date: 08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4359
R;Ancosh, I; Raghavan, N; FitzGerald, P.C.; Scott, A.L.
Gene 164, 261-266, 1995
A;Title: Nucleoside diphosphate kinase from the parasitic nematode Brugia malayi.
A;Reference number: JC4359; MUID:96069592; PMID:7590340
A;Reference number: JC4359; MUID:96069592; PMID:7590340
A;Residues: 1-153 <GHO>
A;Residues: 1-153 <GHO>
A;Residues: 1-153 <GHO>
A;Residues: UNIPROT:P48817; UNIPARC:UPI000012FE9C; GB:U18906; NID:g619942; PIDN
A;Cross-references: UNIPROT:P48817; UNIPARC:UPInding proteins and a role in signal transducts
C;Comment: This enzyme is a pivotal enzyme in the synthesis of nucleotide triphosphates
C;Genetics:
A;Gene: ndk
C;Genetics:
A;Gene: ndk
C;Genetics:
C;Genetics:
A;Gene: ndk
C;Genetics:
A;Genetics:
A;Gene: ndk
C;Genetics:
A;Genetics:
A;Genetics
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Pred. No. 2.9e-45;
3; Mismatches 18;
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Similarity 64.9%;
96; Conservative 33
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C; Species: Drosophila melanogaster
C; Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-C; Accession: $01908
R; Biggs, J.; Tripoulas, N.; Hersperger, E.; Dearolf, C.; Shearn, A. Genes Dev. 2, 1333-1343, 1988
A; Title: Analysis of the lethal interaction between the prune and kille A; Reference number: $01908; MUID:89079007; PMID:2849580
A; Reference number: $01908
A; Molecule type: mRNA
A; Residues: 1-153 <BIG>A; Cross-references: UNIPROT:P08879; UNIPARC:UPI0000011C4; EMBL:X13107; C; Genetics:
A; Gene: awd
A; Cross-references: FlyBase:FBgn0000150
A; Map position: 3 100C-D
C; Superfamily: nucleoside diphosphate kinase
C; Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; pho F; 16-20/Region: ATP binding #status predicted
F; 119/Active site: His (phosphohistidine intermediate) #status predicte
                                                                                                                                                                                                                                                                                               107
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T21354
hypothetical protein F25H2.5 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te:
C; Accession: T21354
R; Wilkinson, J.
submitted to the EMBL Data Library, September 1996
A; Reference number: Z19411
A; Reference number: Z19411
A; Reference number: Z19411
A; Reference number: Z19411
A; Residues: DNA
A; Residues: 1-153 < WIL>
A; Residues: 1-153 < WIL>
A; Cross-references: UNIPROT: Q93576; UNIPARC: UPI000007F
A; Experimental source: clone F25H2
C; Genetics:
A; Gene: CESP: F25H2.5
A; Map position: 1
A; Introns: 18/2; 49/3
C; Superfamily: nucleoside diphosphate kinase
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Pred. No. 1.6e-53;
14; Mismatches 20;
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RESULT 13
533170
nucleoside-diphosphate kinase (EC 2.7.4.6) - garden pea
C; Species: Pieum sativum (garden pea)
C; Species: Pieum sativum (garden pea)
C; Abate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C; Abate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C; Abate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C; Accession: 846513; Millian, sequence determination and heterologous expression of nuclex
A; Reference number: 846513; MulD:94272014; PMID:8003697
A; Accession: 846513
A; Molecule type: mRNA
A; Residues: 1-149 < RIL2>
A; Residues: 1-140 < RIL2>
A; Residue
                             diphosphate kinase phosphoprotein; phosphotransferase; pyrimidir
                                                                                                                                                                                                                                                                                                                                                                                   LVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSV
                                                                                                                                                                                                                                 LERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFFPG
                                                                                                                  Score 510.5; DB 2;
Pred. No. 8.7e-43;
; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152
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S37889
nucleoside-diphosphate kinase (EC 2.7.4.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                  th 63.6%; Sc
Similarity 63.8%; P1
95; Conservative 22;
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ilarity 63.5%;
Conservative 2
by modulating GTP levels
C;Superfamily: nucleoside
C;Keywords: ATP binding; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 94; Conser
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Best Local
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C;Species: Helianthus annuus (common sunflower)
C;Species: Helianthus annuus (common sunflower)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14183
R;Grayburn, W.S.; Vick, B.A.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z17907
A;Accession: T14183
A;Reference number: Z17907
A;Accession: T14183
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-148 <GRA>
A;Residues: 1-148 <GRA>
A;Residues: 1-148 cGRA>
A;Cross-references: UNIPROT:Q96559; UNIPARC:UPI000012FEAB; EMBL:U72142; NID:g1619957;
C;Function:
A;Description: catalyzes transfer of the gamma-phosphate group from ATP to nucleoside cid synthesis, UTP for polysaccharide synthesis, CTP for lipid synthesis and GTP for F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID: 95771347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.7.4.6 [validated, MUID: 20050582]; phosphorylates nucleoside
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DMGRNVCH
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                                                                                                                          61 FFNDLVGYMSSGPVIAMVWEGLDVVKQARQMLGATNPLNSMPGTIRGDFSIQTGRNIVHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFFPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIH
 1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEH--LKQHYIDLKDR
                                                                                           FFPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHG
                                                                                                                                                                                                                                                                                                                                                                                                                        crassa
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicontains: protein kinase
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-C;Accession: T50459
R;Oqura, Y.; Yoshida, Y.; Ichimura, K.; Aoyagi, C.; Yabe, N.; Hasunuma, Eur. J. Biochem. 266, 709-714, 1999
A;Title: Isolation and characterization of Neurospora crassa nucleoside
A;Reference number: Z25071; MUID:20050582; PMID:10583364
A;Reference number: Z25071; MUID:20050582; PMID:10583364
A;Residues: Trellminary; translated from GB/EMBL/DDBJ
A;Residues: 1-154 <OGU>A;Residues: ndk-1
C;Function: <NDK1>
A;Note: ndk-1
C;Function: <PKIN>
A;Description: C2.7.4.6 [validated, MUID:20050582]; phosphorylates nuc;Function: <PKIN>
A;Description: phosphorylates proteins in vitro [validated, MUID:200505A;Note: acts as a signal transducer by phosphorylating proteins
C;Superfamily: nucleoside diphosphate kinase
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: phosphoprotein; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                     - Neurospora
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3.4e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 525;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
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Best Local S
Matches 96
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T50459
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phosphotransferase;

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C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004
C; Accession: S37889; S44519; JN0754; S39174
R; Rasmussen, S.; von Wettstein, D.
submitted to the Protein Sequence Database, March 1994
A; Reference number: S37872
A; Accession: S37889
A; Molecule type: DNA
A; Residues: 1-153 < RAS>
A; Residues: 1-153 < RAS>
A; Experimental source: strain S288C
                                                    ..
H
                                                                                                                                                                   124
                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                              (Saccharomyces
                                                                                          64
                                                                                     VKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVK
                                                                                                                                                                                      Gaps
                                                     .,
H
            Length 149
                                                                                                                                                                                                                                                                                                                                                                             yeast
                                                    Indels
Score 509.5; DB 2;
Pred. No. 1.1e-42;
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                                                  les the NUP100 generate to known proteins
                                                                                                                                                                                                        ; PIDN:CAA53407.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphate kinase;
                                                                                                                                                                                                                                                                                                                                                                                     PIDN: BAA02758.1
                                                                                                                                                                                                                                                                        cerevisiae YNK
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R; Rasmussen, S.W.
Yeast 10, 69-74, 1994
A; 1994
A; Title: Sequence of a 20.7 kb region of yeast chromosome XI includes tip in addition to seven ORFs with weak or no significant similarity to A; Reference number: S44513
A; Accession: S44519
A; Accession: S44519
A; Accession: S44519
A; Accession: S44519
A; Cross-references: UNIPARC; UP10000037234; EMBL: X75780; NID: g433625; PI R; Ekukuchi, T.; Nikawa, J.; Kimura, N.; Watanabe, K.
B; Fukuchi, T.; Nikawa, J.; Kimura, N.; Watanabe, K.
Gene 129, 141-146, 193
A; Title: Isolation, overexpression and disruption of a Saccharomyces ce A; Reference number: UN0754; MUID: 93328116; PMID: 8392963
A; Title: Isolation, overexpression and disruption of a Saccharomyces ce A; Residues: 1-153 <FUK.
A; Accession: JN0754
A; Molecule type: DNA
A; Residues: 1-153 <FUK.
A; Cross-references: UNIPARC: UP10000037234; EMBL: D13562; NID: g433423; PI C; Genetics:
A; Gene: SGD: YNK1; MIPS: YKL067w
A; Gross-references: SGD: S0001550; MIPS: YKL067w
A; Gene: SGD: YNK1; MIPS: YKL067w
A; Genetics:
A; Map position: 11L
C; Function:
A; Description: EC 2.7.4.6 [validated, MUID: 93328116]; nucleoside-diphos C; Keywords: ATP binding #status predicted
E; 119/Active site: His (phosphohistidine intermediate) #status predicted
E; 119/Active site: His (phosphohistidine intermediate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
T08909
hypothetical protein T32A16.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul
C;Accession: T08909
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.
submitted to the Protein Sequence Database, May 1999
A;Reserence number: Z16518
A;Accession: T08909
A;Residues: 1-237 <BEV>
A;Cross-references: UNIPROT:Q8LAH8; UNIPARC:UPI00000ABF3A; EMBL:AL0784
A;Experimental source: cultivar Columbia; BAC clone T32A16
C;Genetics:
A;Gene: ATSP:T32A16.70
A;Map position: 4
A;Introns: 28/1; 74/1; 86/3; 103/3; 159/3; 197/2
C;Superfamily: nucleoside diphosphate kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 505; DB 2; L
Pred. No. 3.1e-42;
28; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAEKEISLWFKPEELVDYKSCAHDWVYE 152
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Similarity 61.5%;
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Best Local Similarity
Matches 91; Conser
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439378781 residues 2443163 seqs, Searched: 2443163 hits satisfying chosen parameters: o£ Total number

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Genesed Database

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a cinted, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.

	uo	mm23-H2 p	Human NM2	Mature hu	Protein d	Human nm2	Н	od	Cyclin-de		O	Tumor met	Human nm2	Protein o	Human NM2	Human nuc	Human MDD	Murine NM	Human pro	Human pro	Human gen	Bovine nu	Bovine nu	Murine NM	Human pro
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AAR11903	AAW62505	AAG79338	ADF76437	ADL82817	ADN05777		ABM81903	ADP54261	ADP23235	ADU06448		ADX05642	ADY19471	ADY14586	ADY81119	AEB11912		ADR66040	AAE21724	AAU69421
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ALIGNMENTS

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M, Tureci
                                                         colon cancer; gastric
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Pfreundschuh M,
            AAY07000 standard; protein; 152
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97US-0061599P.
97US-0061765P.
97US-00948705.
97GB-00021697.
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                                              mm23-H2 protein sequence
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                                   (first
                                                         Cancer associated breast cancer; co. prostate cancer.
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10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
22-JUN-1998;
                                                                                  Homo sapiens
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prostate
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                        AAY07000;
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RESULT 1
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human; lung cancer;

polypeptides products for c acids and property cancers. New isolated cancer associated nucleic using sera from cancer patients, used t diagnosis, monitoring or treatment of c N-PSDB; AAX40201

WPI; 1999-132448/11

isolatedthe

Page 787; 787pp; English. Example 8;

The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically

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Soriasis;
binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
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in screening for
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Pred. No. 6.1
; Mismatches
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ETH ZUERICH ETH ZENT
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2000US-0199312P
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ses 152; Conser
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                                                                                                                          Sequence 152
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24-APR-2000;
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therapeutic
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                                                                                                   lung cancer
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                                                                                                                                                                     Matches
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This invention describes a novel use of the NM23 protein family, analysis, diagnosis, prevention and/or treatment of skin or intediseases and/or wound healing and/or associated pathological

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disturbances. The products of the invention have vulnerary, antitumour, gastrointestinal, dermatological, anti-inflammatory and antiulcer activity. The NM23 protein family act as nucleotide-diphosphate kinases, DNA-binding and transcription activating agents and regulators of Rascribes. The proteins of the invention, antibodies (Ab) directed against them, and their encoding nucleic acids, or related vectors, transformed cells and antisense sequences, are used for analysis, diagnosis, prevention and/or treatment of skin and intestinal diseases (where associated with uncontrolled tissue growth or cell differentiation, particularly skin and intestinal tumours, also psoriasis, Crohn's disease of and ulcers), wound healing and/or associated pathological alterations). They are also used to screen for agents that are potentially useful for treating these conditions. In vitro monitoring of NM23 protein expression in tissue samples provides an early diagnosis of disease. This sequence represents the human NM23B protein described in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metastatic potential; familial breast cancer
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Pred. No. 6.1e-90;
Mismatches 0;
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assessment of aggressiveness
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91US-00806932.
95US-00475684.
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N-PSDB; AAI72922.
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11-DEC-1991;
07-JUN-1995;
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alteratio
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                                                               genetic
The sequences given in AAG79335-38 show the related human proteins M and H2S. These proteins are products of different genes, with NM23 being localised to chromosome 17. These proteins are used to predict aggressiveness (metastatic potential) of human tumours and in genetic tests for cancer susceptibility, diagnosis and prognosis, also for selection of treatment, e.g. susceptibility to early-onset familial breast cancer. Gene nm23 may contribute to tumourigenicity and alterin its regulation may be an early stage in the metastatic cascade.

Allelic or homozygous deletion of the gene is detected in some priman
                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                             Sequence 152
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 Length 152
                 Indels
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 803; DB 5;
No. 6.1e-90;
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                 Mismatches
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RESULT 4 ABU89707

ABU89707 standard; protein; ABU89707

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152

entry) (first 10-JUL-2003 cardiovascular disease in expressed differentially Protein

oris; al; Cardiovascular disease; arteriosclerosis; ischaemia; angina pect myocardial infarction; cardiant; antiarteriosclerotic; antiangin gene therapy; differential gene expression.

sapiens Ношо

WO2003031650-A2

17-APR-2003.

2002WO-EP011034 02-OCT-2002; 2001GB-00024145 08-OCT-2001;

BAYER AG (FARB) Σ Wick Σ Gehrmann Σ Munnes

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-403108/38 N-PSDB; ACA89880 2003

e.g. detection angina, ischemia, myocardial infarction or arteriosclerosis by of a polynucleotide in a biological sample comprises detecting hybridization complex.

Claim 3; Page 251-252; 454pp; English

prognosing biological t The invention describes a method of predicting, diagnosing or pra cardiovascular disease by detection of a polynucleotide in a ksample comprises hybridising at least one of the polynucleotide nucleic acid material of a biological sample, thus forming a hybridisation complex, and detecting the hybridisation complex.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in
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      reagent
polynucleotides, polypeptides, antisense molecule, antibody and reagent are useful for preparing compositions for preventing, predicting or diagnosing, or a medicament for treating a cardiovascular disease, e.g. arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction. This sequence represents a protein identified in the invention a being differentially expressed in individuals with cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ind inhibits tyrosine kinase activity to the test compound and measuring in of the measured proteins or mRNA
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine kinase activity, type 1 plasminogen activator inhibitor; I TIMP-1; tissue inhibitor of metalloproteinase 1; vinculin, vascular endothelial growth factor; VEGF; placental growth factor; migration inhibitory factor; MIG; human; nm23-H2.
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                                                                                                                                                                                                                   Score 803; DB 6;
Pred. No. 6.1e-90;
Mismatches 0;
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a mammal by exposing
mammal the level of a
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N-PSDB; ADH17090.
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                                                                                                                                                                         Sequence 152 AA;
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24-FEB-2003;
24-FEB-2003;
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Best Local S
Matches 152
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metalloproteinase 1), vinculin, vascular endothelial growth factor (VEGF), placental growth factor (PLGF), VEGF/PLGF heterodimers or migration inhibitory factor (MIG), exposing the mammal to the test compound and then measuring in the mammal the level of at least one of the proteins and/or mRNA transcripts previously measured. The method of the invention may be useful for determining whether a test compound inhibits tyrosine kinase activity in a mammal. The current sequence is that of the tyrosine kinase activity inhibition-related protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
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                                                                                                                                                                                                                                                             Tumour-associated antigenic target; TAT; human; overexpression; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
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                                                                                                                                                                                                            MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDL
                                                                                                                                                                                                                          New tumor-associated antigenic target polypeptides and nucleic useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour-associated antigenic target (TAT) polypeptide PRO3637,
                                                                                                                                                         Length 152
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6.1e-90;
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                                                                                                                                                                                Mismatches
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                                                                                                                                                         Score 803;
Pred. No. 6
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B; ACN40229.
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                                                                                                                                                                      al Similarity
152; Conser
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                                                                                                                                 Sequence 152 AA;
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(TAT)

The invention relates to human tumour-associated antigenic targe polypeptides, and their related nucleic acids. The TAT polypepti

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coverexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides, expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT nucleic and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, ovarian cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
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erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated
renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
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Pred. No. 6.1e-90;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome identification and in gene therapy. represents a TAT polypeptide of the invention
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152; Conservative
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N-PSDB; ADP23161.
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                                         The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, costeopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polypublication of the invention may have a use in gene therapy. The PRO polypeptide, its of agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, indiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythem multiforme, contact dermatitis, psociasis, an allergic disease, erythem multiforme, contact dermatitis, psociasis, an allergic
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This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers.

The cdk modulator is preferably N-5-[[5-(1,1-Dimethylethyl)-2-coxazolyl]methyl]thiol-2-thiazolyl-4-piperidine carboxamide, 0.5-L-cartaric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences. This sequence represents a biomarker used in the method of the invention.
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                                                                                                                                           The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody composition, and method are useful for diagnosing and treating a related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antiinflammatory; Immune disorder; Dermatological; Immunosuppres Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemi Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
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6.1e-90;
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Pred. No. 6
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polypeptide.
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otide, useful for diagnosing and e.g. systemic lupus erythematosus thyroiditis, or diabetes mellitum
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                                                                                                                                                         The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a PRO polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                            Length 152;
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100.0%; Pred. No. 6.1e-90;
live 0; Mismatches 0;
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nucleotide phosphodiesterase. The invention may be useful for the development of compounds with a cytostatic activity acting as human-PRUNI overexpression inhibitors. The invention is useful for preparation of medicaments in the treatment of tumor metastases, for example breast carcinoma, sarcoma, neuroblastoma, prostate tumor, pancreatic tumor, colonic tumor, rectal tumor, medulloblastoma, epitelioma, epatocarcinoma, the h-PRUNE posses cyclic nucleotide phosphodiesterase activity with preferential activity for camp over cGMP, the h-PRUNE overexpression can be effectively suppressed by certain PDE inhibitors thus the PDE inhibitor provides an effective alternative therapy for cancer treatment. The present sequence is that of the h-PRUNE protein which was used during the development of the novel method of the invention.
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91US-00806932
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N-PSDB; AAA70315.
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11-DEC-1991;
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Claim 1; Fig

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The invention relates to an isolated polynucleotide molecule encoding a human nm23 protein comprising nm23-H1 having a sequence of 746 base pairs (bp) fully defined in the specification or nm23-H2S having a sequence of 670 bp fully defined in the specification. The polynucleotide molecule of the invention is useful as a diagnostic tool for detecting and/or determining RNA or DNA which can be employed to detect mRNA expression in cancer cells to aid in predicting the malignant potential of a human tumour. The DNA and the antibodies may also be used to detect
The present sequence is the human nm23 protein nm23-H2S. Its coding sequence was isolated by searching a human lung cDNA library for sequences similar to pnm23-H2. Nm23 proteins are involved in tumour metastasis, and this protein, its gene and antibodies can be used to determine an individual's susceptibility to cancer and the likelihood of tumour metastasis within that individual. This is possible using a number of methods, including Northern blotting, nuclease protection assays, in situ hybridisation, immunohistochemical analysis and solid phase
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                                                                                                                                                                                                                                                                                        encoding a human nm23 protein useful for predicting al of a tumor and the genetic predisposition for t, comprises nm23-H1 and nm23-H2s genes.
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Pred. No. 7.6e-90,
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of potential
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N-PSDB; AAL53615.
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152; Conser
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       genetic predisposition for developing cancer. The human nm23 protein be employed to produce nm23 antibodies. This sequence represents the -H2S protein of the invention
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predicting
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                                                               Length 176
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 aid in
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cells to
                                                              Score 803; DB 5;
Pred. No. 7.6e-90;
); Mismatches 0;
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/label= Mature NM23-H2S
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  9
                                                                                                                                                                                                                                                                                                                      NM23-H1; NM23-H2S; aggressiveness; cancer susceptibility; early-onset
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of DNAs in normal
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                                             Sequence 176 AA;
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abnormalities
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11-DEC-1991;
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US-10-074-694-3 876 Title:

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residues 0.5 6736768 Gapext 51470 seqs, Searched: hits satisfying chosen parameters: of. number Total

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a inted, No. is the number of results predicted by chance to have greater than or equal to the score of the result being proderived by analysis of the total score distribution. Pred. No. score gand is

SUMMARIES

Description	Sequence 49,	equence 1577	equence 966,	e 994,	equence 411(e 118,	equence 1820	42,	49,	equence 4834	009	342	2, 1	202	equence 107	equence 31,	equence 609;	4	-	œ	equence 9, App	, Ap	, App	equence 1574,	Sequence 12, Appl
ΩI	878-556A-4	1-234-1	US-11-055-822-966	- 99	US-10-467-657-4110	US-10-763-712A-118		US-11-090-439-42	US-10-770-726-49	-4	US-10-995-561-600	2	US-11-091-334-2	-10-793-626-20	US-10-878-556A-107	US-11-143-980-31	-467-	US-10-467-657-7548	US-10-510-386-42	US-11-055-822-408	-978-	80-991-7	US-11-051-267-16	-10-821-234-1	US-10-510-386-12
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-10-467-657-2 -10-467-657-6 -10-763-712A-	US-10-763-712A-99 US-11-069-642-22 US-10-467-657-764	-10-878-556A-1 -11-129-143-17 -10-793-626-26	-10-508-263-1	10-467 11-059	-10-67-296-3 -10-667-295-71 -10-623-155-35	US-10-763-712A-15 US-11-074-176-142 US-10-131-826A-138 US-11-174-150-27
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US-10-821-234-1577; Application US/10821234; Sequence 1577, Application US/10821234; Publication No. US20050255114A1; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan; Applicant, Birgit; APPLICANT: Andarmani, Susan; APPLICANT: Andarmani, Susan; APPLICANT: Tang, Y. Tom; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
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Pred. No. 3.3e-72;
3; Mismatches 6;
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                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/ndka_human
; DATABASE ENTRY DATE: 1990-04-01
US-10-878-556A-49
RESULT 1
US-10-878-556A-49
; Sequence 49, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein exp;
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SEQ ID NO 49
; LENGTH: 152
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APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
                                                                                                                                                                                            Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See File Wrapper
                                                                                                                                                                                                                         Indels
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Pred. No. 4.3e-69
; Mismatches
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1577
LENGTH: 152
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CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931415.2
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R FILING DATE: 1999-07-08
R APPLICATION NUMBER: DE 19931418.7
R FILING DATE: 1999-07-08
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1-055-822-966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/11055822
5. US20050260707A1
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1 Similarity 90.1%;
137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Pompejus, Marn-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior Application
SEQ ID NOS: 1158
                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-821-234-1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-055-822-966; Sequence 966, A; Publication No.
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ENGTH: 136
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                                                                                               SERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFFTG
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APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gregor
APPLICANT: Edder, Ogkar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2006-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-08
                              42;
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Pred. No. 4.9e-28;
1; Mismatches 42;
  Score 333.5; DB Pred. No. 4.9e-28
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OR APPLICATION NUMBER: DE 19931418.7

OR FILING DATE: 1999-07-08

OR APPLICATION NUMBER: DE 19931419.5

OR FILING DATE: 1999-07-08

OR APPLICATION NUMBER: DE 19931420.9

OR FILING DATE: 1999-07-08

A PILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                    publication No. US20050260707A1; GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Krozz
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larity 49.2%;
Conservative
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NUMBER OF SEQ ID
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Sequence 42, Application US/11090439
Publication No. US20050266442A1
GENERAL INFORMATION:
APPLICANT: Squillace, Rachel
APPLICANT: Weiner, Michael P.
TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Thereof
FILE REFERENCE: 24318-502
CURRENT APPLICATION NUMBER: US/11/090,439
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: 60/556,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETNPADSKPGTIRGDFCI-----QVGRNIIHGS-DSVKSAEKEISLWFQPE--
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                                   TFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEH--
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APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
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 61;
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                                                                                                                             GAISRVINNADL-LYGKAKELYEANKDLLKGTNP
                                                                                                                                                                          157
 Mismatches
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CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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SEQ ID NO 1820
LENGTH: 1144
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26;
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 Conservative
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US-10-467-657-1820
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Best Local S
Matches 37
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FYAGL
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APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
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No. 1.2;
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GENERAL INFORMATION:
APPLICANT: Solazyme, Inc.
APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions; TITLE OF INVENTION: Production
FILE REFERENCE: H2042101-CIP
CURRENT APPLICATION NUMBER: US/10/763,712A
CURRENT FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: US 10/287,750
PRIOR FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: US 10/411,910
                                                                                                                                                                                                                                                                                        US/10/467,657
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 4110
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Pred.
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Sequence 4110, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patentin version 3.2
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nes 60; Conser
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ENGTH: 428
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ADSKPGT--IRGDFCIQVGRNIIHGSDSVK---SAEKEISLW--FQPEELVEYK
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         APPLICANT: FONTANA Maria Kilca
APPLICANT: PIZZA Mariagrazia
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 4834
LENGTH: 293
                                                                                                                                                                                                                                                                                                 Length 293;
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Pred. No. 5.1;
7; Mismatches
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5. US20050245730A1
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                                                                                                                                                                                                                                                  ; ORGANISM: Neisseria gonorrhoeae US-10-467-657-4834
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ilarity 25.0%;
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US-10-995-561-600
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LENGTH: 2261
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                                                                                                                                                                                                         -LVGLKFLQASEDLLKEHYTDLKDRPFFTGLV
                                                                                                                                                                          29;
                                                                                                                                            Length 1302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING,
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 795;
                                                                                                                                                                         Indels
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                                                                                                                                  n. Similarity 23.7%; Score 69.5; l
. Similarity 23.7%; Pred. No. 24;
36; Conservative 29; Mismatches
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Pred. No.
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Publication No. US20050260581A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 49, Application US/10770726 Publication No. US20050266409A1 GENERAL INFORMATION:
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      2004-03-2
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PRIOR FILING DATE: 2004-0
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2
SEQ ID NO 42
LENGTH: 1302
                      : 62
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                                                                                          ; ORGANISM: Homo sapiens
US-11-090-439-42
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Best Local S
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APPLICANT: Watanabe, Calin K
APPLICANT: Watanabe, Calin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT FILING DATE: 2002-04-24
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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larity 24.2%; Pred. No. 9.
Conservative 23; Mismatche
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 550
EQ ID NO 342
LENGTH: 364
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APPLICATION NUMBER: 60/(FILING DATE: 1997-09-19
                                                                                                                                                                     Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy ?
Tumas, Daniel
                                                                                                                                  Gerritsen, Mary E
                  Baker, Kevin P.
Beresini, Maureen
Deforge, Laura
                                                                        Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
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-10-131-826A-342
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Pred. No. 9.7;
23; Mismatches
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIL
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2050
LENGTH: 428
                                                                      APPLICANT: Soppet, et al.

TITLE OF INVENTION: Growth Factor HTTER36
FILE REFERENCE: PF230P1
CURRENT APPLICATION NUMBER: US/11/091,334
CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: 60/557,393
PRIOR FILING DATE: 2004-03-30
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: 09/357,905
PRIOR FILING DATE: 1999-07-21
PRIOR FILING DATE: 1999-07-21
PRIOR FILING DATE: 1997-03-26
PRIOR FILING DATE: 1997-03-26
PRIOR APPLICATION NUMBER: 60/014,098
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Pred. No. 1
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Publication No. US20050255478A1
GENERAL INFORMATION:
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-11-091-334-2
Sequence 2, Application US/11091334
Publication No. US20050244867A1
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ilarity 24.2%;
Conservative 23
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NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
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                                                       GENERAL INFORMATION:
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---FTHKKPLPKFLTL----FAGPLFNFILALVLFIGLAYYQGTPTNVIGEVV- 208
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                                                                      --IMANSERTF--IAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQ 56
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  48;
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Publication No. US20050266399A1;
GENERAL INFORMATION:
APPLICANT: Hoffmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated protein expression;
FILE REFERENCE: 21762;
CURRENT APPLICATION NUMBER: US/10/878,556A;
CURRENT FILING DATE: 2004-06-28;
NUMBER OF SEQ ID NOS: 199;
SOFTWARE: Patentin version 3.1;
SEQ ID NO 107;
LENGTH: 1101
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; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw hum/acly_human
; DATABASE ENTRY DATE: 1996-10-01
US-10-878-556A-107
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Best Local Similarity 22.6%; Pred. No. 73;
Matches 43; Conservative 26; Mismatches
  Mismatches
  19;
  Conservative
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US-10-074-694-3 876 1 QSQPAVKPCHLKG score: Perfect Title:

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SUMMARIES

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8	9	91.	S	m	-09-791-11	equence 2, Appl	
m	798	<u>.</u>	152	ស	3-1311	e 13111	
4	g	0	7	വ	-10-732-923-1	e 13112,	
Ŋ	S	0	7	ო	-09-833-790-42	e 426, Ap	
9	ð	0	8	ស	-10-732-923-1	equence 13340,	
7	g	0	Ø	ø	US-11-013-684-2	2, Appl	
8	g	0	æ	9	-037-71	42, App	
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10	74.	8	7	4	-10-288-798-1	19, App	
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12	74.	ω.	7	Ŋ	-9	e 13342,	
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16	S	9	5	ហ	-10-370-	equence 110, Ap	
17	ហ	9	ហ	വ	-10-732-923-1334	e 13341,	
18	S	9	S	വ	3-13	equence 13355,	
19	S	9	S	4	ī	pp_1	
20	S	9	152	Ŋ	9	e 13353,	
21	S	5	152	4	-10-133-62	equence 21, App	
22	4	IJ.	151	Ŋ	2-923-	equence 13354,	
23	4	5	152	4	2	equence 3, Appl	
24	•	т М	153	ស	US-10-732-923-13132	equence 13132,	
25	72	щ	152	ო	US-09-791-118A-3	equence 3, Appl	
26	2	ო	152	4	-10-232-188-5	equence 5, Appl	
27	N	ო	152	4	US-10-133-628-12	d	

or for

equence 90, Ap equence 13345,	, А 46,	equence 1 equence 4	127, App	equence 332, A	13113,	, App	13320,	13128,	equence 13336,	334,	equence 13117,	•	~
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Sequence 2, Application US/09791118A

Patent No. US20020034741A1

GENERAL INFORMATION:

APPLICANT: Werner, Sabine

APPLICANT: Braun, Susanne

APPLICANT: Penzberg, Jorn-Peter

APPLICANT: Regenbogen, Johannes

TITLE OF INVENTION: Use of polypeptides or nucleic acids

TITLE OF INVENTION: encoding these of the gene family NM23 for the

TITLE OF INVENTION: treatment of skin or intestinal disorders, and

TITLE OF INVENTION: the identification of pharmacologically
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                                                                                          PHENOTYPES
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                                                                                          IMPROVED
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Pred. No. 3.3e-88;
0; Mismatches 0;
                      Sequence 13110, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH I
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13110
; LENGTH: 166
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; Sequence 13111, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796) C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13111
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       FILE REFERENCE: 50125/012002
CURRENT APPLICATION NUMBER: US/09/791,118A
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 60/199,312
PRIOR FILING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: DE 100 08 330.7
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Fast SEQ for Windows Version 4.0
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Matches 152; Conser
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GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 13112
LENGTH: 176
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Mismatches 10
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; Sequence 426, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Wohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCI;
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SEQ ID NO 426
; LENGTH: 178

***CONTRACT OF THE CONTRACT OF 
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Pred. No. 4
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illarity 91.5%;
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1 Similarity 91.5%;
150; Conservative
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US-09-833-790-426
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Best Local Similarity
Matches 150; Conser
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US-09-833-790-426
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TITLE OF INVENTION: Biomakers for Liver Diseases and Method for
FILE REFERENCE: 04P0019
CURRENT APPLICATION NUMBER: US/11/013,684
CURRENT FILING DATE: 2004-12-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.2
                                                               IMPROVED PHENOTYPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 180;
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Pred. No. 4.2e-79;
1; Mismatches 10;
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Pred. No. 4.2e-79,
1; Mismatches 10
US-10-732-923-13340
; Sequence 13340, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH I
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13340
; LENGTH: 180
                                                                PLANTS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/11013684 Publication No. US20050136489A1 GENERAL INFORMATION:
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nilarity 91.5%;
Conservative
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11 Similarity 91.5%;
150; Conservative
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; ORGANISM: HOMO &
US-10-732-923-13340
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; ORGANISM: Human
US-11-013-684-2
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LENGTH: 180
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Best Local S
Matches 150
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US-11-037-713-42

RESULT

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US-10-732-923-13126

Sequence 13126, Application US/10732923

Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-15 (52796) C

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT FILING DATE: 2003-12-10

PRIOR FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 13126

LENGTH: 152
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No. 1.5e-77;
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Pred. No. 4.2e-79
1; Mismatches 1
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                                              APPLICANT: JACQUEMIER, JOCELYNE
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: TAGETT, REBECCA
TITLE OF INVENTION: PROCENOSIS
FILE REFERENCE: 1016-R-04(B)
CURRENT APPLICATION NUMBER: US/11/037,713
CURRENT FILING DATE: 2005-01-18
PRIOR FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 3.3
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Sequence 42, Application US/11037713
Publication No. US20050221398A1
GENERAL INFORMATION:
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llarity 91.5%;
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larity 96.7%;
Conservative
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US-10-732-923-13126
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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147; Conser
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Best Local Similarity
Matches 150; Conser
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                                                                                                                                                                                                                                                                                             SEQ ID NO 42
LENGTH: 180
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Best Local S
Matches 147
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Application US/10362892 to. US20040038881A1
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iilarity 90.2%;
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 Sequence 19, Application Publication No. US200-GENERAL INFORMATION:
APPLICANT: INCYTE GENERAL APPLICANT: HAFALIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 147; Conser
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LENGTH: 177
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OTHER INFORMATION: Incyte ID No. US20030207299A1 7274927CD1
                                                                                                                                                                                   GENEKAL INCAMATION:
GENEKAL INCAMATION:
GENEKAL INCAMATION:
GENEKAL INCAMATION:
APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
APPLICANT: GURURAJAN, Rajagopal; DING, Li;
APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
APPLICANT: HORNTON, Michael, ELLIOTT, Vicki S.;
APPLICANT: LU, Yan; ISON, Craig H.;
APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
APPLICANT: RARNEY, Liam; POLICKY, Jennifer L.;
APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
TITLE OF INVENTION NUMBER: US 60/240,542
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,542
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 774.5; DB 4
Pred. No. 5.8e-77;
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121 DSVESAEKEISLWFQPEELVDYKSCAQNWIYE
                                                                                                                     Sequence 19, Application US/10288798
Publication No. US20030207299A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS
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147; Conser
                                                                                             US-10-288-798-19
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,US-10-362-892-19
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LENGTH: 177
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Best Local
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123
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OTHER INFORMATION: Incyte ID No. US20040038881A1 7274927CD1
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GENERAL LINGUERATION
GENERAL LINGUERAL LINGUER
GENOMICS, INC.; BANDMAN, Olga
APPLICANT: NGUYEN, Danniel B.; WALIA, Narinder K.
APPLICANT: GANDHI, Amena R.; GRURAJAN, Rajagopal
APPLICANT: GANDHI, Amena R.; GRURAJAN, Rajagopal
APPLICANT: TRIBOULEY, Cacherine M.; THORNTON, Michael
APPLICANT: TRIBOULEY, Cacherine M.; THORNTON, Michael
APPLICANT: ELLIOTT, Vick! S.; LU, Yan
APPLICANT: ELLIOTT, Vick! S.; LU, Yan
APPLICANT: SURBILL, John D.; MARCUS, Gregory A.
APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
APPLICANT: LING, Preeti G.; RAMKUMAR, Jayalaxmi
APPLICANT: BURRELL, John D.; MARCUS, Liam
APPLICANT: BURRORD, Neil
APPLICANT: BURRORD, Neil
APPLICANT: BURRORD, Neil
APPLICANT: BURRORD, Neil
APPLICANT: BURRORD, Neil
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APPLICANT: BURRORD, Neil
APPLICANT: BURRORD, Neil
APPLICANT: BURRORD, Neil
APPLICANT: BURRORD, Neil
APPLICANT: BURRORD, NUMBER: US 60/229, 873
PRIOR APPLICATION NUMBER: US 60/231, 357
PRIOR PILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: US 60/234, 902
PRIOR APPLICATION NUMBER: US 60/234, 902
PRIOR APPLICATION NUMBER: US 60/234, 902
PRIOR APPLICATION NUMBER: US 60/236, 499
PRIOR APPLICATION NUMBER: US 60/234, 902
PRIOR APPLICATION NUMBER: US 60/236, 499
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/234, 902
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/234, 992
PRIOR APPLICATION NUMBER: US 60/234, 992
PRIOR APPLICATION NUMBER: US 60/234, 992
PRIOR APPLICATION NUMBER: US 60/234, 992
                                                                                                                                                                                                                   THORNTON, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kavitha
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NUMBER OF SEQ ID NOS: 48
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-10-732-923-13342
; Sequence 13342, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
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15 MANSERTFIAIKPDGVORGLVGEIIKRFEOKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
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                                                                             US-10-232-188-4

US-10-232-188-4

Sequence 4, Application US/10232188

Publication No. US20030022306A1

GENERAL INFORMATION:

Hawkins, Phillip R.

TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 2.4e-75;
3; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/713,825
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,188
FILING DATE: 28-Aug-2002
PRIOR APPLICATION DATA:
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-10-133-628-11
; Sequence 11, Application US/10133628
; Publication No. US20030207830A1
; GENERAL INFORMATION:
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MEDIUM TYPE: Diskette
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larity 94.1%;
Conservative
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                                                                                                                                                                                                                                                                                                       COUNTRY: U.S. ZIP: 94304
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143; Conser
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Best Local S
Matches 143
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APPLICANT: Goppelt, Andreas
APPLICANT: Goppelt, Andreas
APPLICANT: Regenbogen, Johannes
TITLE OF INVENTION: Use of polypeptides or nucleic acids
TITLE OF INVENTION: treatment of skin or intestinal disorders, and
TITLE OF INVENTION: the identification of pharmacologically
TITLE OF INVENTION: active substances
FILE REFERENCE: 50125/012002
CURRENT APPLICATION NUMBER: US/09/791,118A
CURRENT APPLICATION NUMBER: US 60/199,312
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-02-23
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TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 13342
LENGTH: 177
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Pred. No. 5.8e-77;
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Pred. No. 2.4e-75
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### APPLICANT: GALLOIS-MONTBRUN, SARAH

APPLICANT: SCHNEIDER, BENOIT

APPLICANT: SCHNEIDER, BENOIT

APPLICANT: GLACOMONI-FERNANDES, VERONIQUE

APPLICANT: DEVILLE-BONNE, DOMINIQUE

TITLE OF INVENTION: MUTANT NDP KINASES FOR ANTIVIRAL NUCLEOTIDE ANALOG

TITLE OF INVENTION: ACTIVATION AND THERAPEUTIC USES THEREOF

TITLE OF INVENTION: ACTIVATION NUMBER: US/10/133,628

CURRENT APPLICATION NUMBER: US/10/133,628

CURRENT PAPLICATION NUMBER: US/10/133,628

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTING DATE: 2002-04-29

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTING DATE: 2002-04-29

NUMBER OF SEQ ID NO 11

ENGTH: 152

TYPE: PRT

ORGANISM: Homo sapiens

US-10-133-628-11

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US-09-134-001C-3216

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RESULT 1

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Sequence 5, Application US/08713825

Patent No. 5874285

APPLICANT: Bandman, Olga

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc. STRES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc. STRES:

COUNTRY: U.S.

COUNTRY: U.S.

ZIP: 94304

COMPUTER: EAA ALC

COUNTRY: U.S.

CONFUTER: EARL SEQ Version 1.5

CONFUTER: IBM Compatible

COMPUTER: IBM COMPATA:

MAPPLICATION NUMBER: US/08/713,825

FILING DATE: Filed Herewith

PRIOR PAPLICATION NUMBER: US/08/713,825

FILING DATE: Filed Herewith

APPLICATION NUMBER: 36,749

RECISTRATION NUMBER: 36,749

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Pred. No. 1.6e-91
Mismatches 0
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APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
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Pred. No. 1.6e-91;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
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US-09-199-842-5
; Sequence 5, Application US/09199842
; Patent No. 6087125
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
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                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE:
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Pred. No. 1.6e-91
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Patent No. 6486300
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE
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STREET: 3174 Porter Drive
CITY: Palo Alto
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APPLICATION NUMBER: US/09/460,532
FILING DATE: 13-Dec-1999
PRIOR APPLICATION DATA:
                                                                                                                                              APPLICANT: Charles R. King
APPLICANT: Charles R. King
APPLICANT: Patricia S. Steeg
APPLICANT: Lance A. Liotta
TITLE OF INVENTION: PRODUCTION AND USE OF HU
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
FILE REFERENCE: 14014.0321
CURRENT APPLICATION NUMBER: US/09/335,948
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 07/806,932
PRIOR FILING DATE: 1991-12-11
PRIOR APPLICATION NUMBER: 07/422,801
PRIOR FILING DATE: 1989-10-18
NUMBER OF SEQ ID NOS: 6
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
                                                                               Sequence 1, Application US/09335948
Patent No. 6329198
GENERAL INFORMATION:
APPLICANT: National Institutes of 1
APPLICANT: Charles R. King
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TER READABLE FORM:
MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS
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US-09-335-948-1
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152; Conser
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US-07-806-932B-3
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SEQ ID NO 2
LENGTH: 176
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; ORGANISM: HO
US-09-335-948-2
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US-09-335-948-2
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Best Local S
Matches 152
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Sequence 987, Application US/09538092

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P22392
US-09-538-092-987
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Pred. No. 1.6e-91;
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Pred. No. 1.6e-91;
Mismatches 0;
          FILING DATE: <Unknown>
APPLICATION NUMBER: 08/713,825
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
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APPLICATION NUMBER: US/09/199,842
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                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CLONE: 127983
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LENGTH: 152
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 152; Conser
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Best Local Similarity
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US-09-538-092-987
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Sequence 2, Application US/09335948

Patent No. 6329198

GENERAL INFORMATION:

APPLICANT: National Institutes of Health
APPLICANT: Charles R. King
APPLICANT: Patricia S. Steeg

APPLICANT: Lance A. Liotta

TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN

TITLE OF INVENTION: AND ANTIBODIES THEREFOR
FILE REFERENCE: 14014.0321

CURRENT APPLICATION NUMBER: US/09/335,948

CURRENT FILING DATE: 1999-06-18

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1991-12-11

PRIOR FILING DATE: 1991-12-11

PRIOR FILING DATE: 1999-10-18

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

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AND ANTIBODIES
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Pred. No. 1.9e-91;
Mismatches 0;
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PROTEIN
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CECCHI & STEWART
BECKER FARM ROAD
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APPLICANT: KING, ET AL.
TITLE OF INVENTION: HUMAN NM23 PRO:
TITLE OF INVENTION: THEREFOR
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larity 100.0%;
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TITLE OF INVENTION: HUMP
TITLE OF INVENTION: THEN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BY
ADDRESSEE: CECCHI & ST
STREET: 6 BECKER FARM
CITY: NEW JERSEY
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US-08-713-825-4
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Best Local S
Matches 134
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APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e-91;
Matches 152; Conservative 0; Mismatches 0;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                          APPLICATION NUMBER: 07/422,801
FILING DATE: 18 october 1989
ATTORNEY/AGENT INFORMATION:
NAME: CAPELLO, SUSAN A.
REGISTRATION NUMBER: 34,560
REFERENCE/DOCKET NUMBER: 469200-72
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1700
                                                                    SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/806,932B
FILING DATE: 11 december 1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,801
                                                                                                                                                                                                                                                                                                                                  176 AMINO ACID RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PE: Diskette
IBM Compatible
SYSTEM: DOS
FastSEQ Version 1.5
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ORIGINAL SOURCE: HUMAN NM 23-H2S
          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
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Patent No. 5874285
GENERAL INFORMATION:
                                                         PC-DOS
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RELEVANT RESIDUES IN SEQUIS-07-806-932B-3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Ver
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                                          IBM PS/2
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                                                          OPERATING SYSTEM:
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                                           COMPUTER:
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APPLICANT:
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STATE:
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Pred. No. 3.2e-81;
); Mismatches 8;
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APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
                                                                                                                                                   PF-0124 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: U.S. ZIP: 94304
              US/08/713,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,
FILING DATE:
         APPLICATION NUMBER: US/08/713, FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J. REFERENCE/DOCKET NUMBER: PF-0: TELEPHONE: 415-85-0555 TELEPHONE: 415-845-4166 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 152 amino acids TYPE: amino acids
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Patent No. 6087125
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
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larity 88.2%;
Conservative
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APPLICATION DATA
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134; Conser
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LIBRARY: GenBa
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; Sequence 4, Application US/09335948
; Patent No. 6329198
; GENERAL INFORMATION:
; APPLICANT: National Institutes of Health
APPLICANT: Charles R. King
; APPLICANT: Lance A. Liotta
; TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
; TITLE OF INVENTION: AND ANTIBODIES THEREFOR
; TITLE OF INVENTION: AND ANTIBODIES THEREFOR
; FILE REFERENCE: 14014.0321
; CURRENT APPLICATION NUMBER: US/09/335,948
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 07/806,932
; PRIOR FILING DATE: 1991-12-11
; PRIOR FILING DATE: 1991-12-11
; PRIOR FILING DATE: 1989-10-18
; NUMBER OF SEQ ID NOS: 6
; SOFTHARE: FABELSEQ for Windows Version 4.0
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Pred. No. 3.2e-81;
0; Mismatches 8;
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Pred. No.
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TELECOMMUNICATION INFORMATION
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illarity 88.2%;
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1 Similarity 88.2%;
134; Conservative
                                                                  LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 468542
             TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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134; Conser
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PRT
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Best Local S
Matches 134
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                                                                                                                                                                        PROTEIN
                                                                                           TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROJ
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .. 8
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Pred. No. 3.2e-81
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/199,842
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/713,825
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,532
FILING DATE: 13-Dec-1999
PRIOR APPLICATION DATA:
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SEQUENCE DESCRIPTION: SEQ ID NO: US-09-460-532-4
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US-09-538-092-933
; Sequence 933, Application US/09538092
                                                               RESULT 11
US-09-460-532-4
; Sequence 4, Application US/09460532
; Patent No. 6486300
; GENERAL INFORMATION:
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Best Local Similarity 88.2%; Pr
Matches 134; Conservative 10;
                                                                                                                                                                                                                                                                                                                                 Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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ULE TYPE: peptide
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ADDRESSEE:
ADDRESSEE:
STREET: 6
CITY: ROSE:
STATE: NEW
COUNTRY: U
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INFORMATION F
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US-07-806-
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Sequence 5, Application US/09335948

Patent No. 6329198

GENERAL INFORMATION:

APPLICANT: National Institutes of Health

APPLICANT: Charles R. King

APPLICANT: Dance A. Liotta

TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN

TITLE OF INVENTION: AND ANTIBODIES THEREFOR

TITLE OF INVENTION: AND ANTIBODIES THEREFOR

FILE REFERENCE: 14014.0321

CURRENT APPLICATION NUMBER: US/09/335,948

CURRENT FILING DATE: 1999-06-18

PRIOR FILING DATE: 1995-06-07

PRIOR PILING DATE: 1995-06-07

PRIOR FILING DATE: 1991-12-11

PRIOR PILING DATE: 1999-10-18
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        GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Giot, Loic

APPLICANT: Giot, Loic

TITLE OF INVENTION: Protein-Protein Complexes and Method of

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/178,965

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

SEQ ID NO 933

LENGTH: 152
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                                                                                                                                                                                                                                                                                                                                                                    89.7%; Score 720; DB 2; 1 larity 88.2%; Pred. No. 3.2e-81; Conservative 10; Mismatches 8;
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Pred. No. 4.2e-81
10; Mismatches
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-335-948-5
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/806,932B
FILING DATE: 11 december 1991
CLASSIFICATION: 530
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R: 469200-72
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APPLICATION NUMBER: 07/422,801
FILING DATE: 18 october 1989
ATTORNEY/AGENT INFORMATION:
NAME: CAPELLO, SUSAN A.
REGISTRATION NUMBER: 34,560
REFERENCE/DOCKET NUMBER: 469200-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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ORIGINAL SOURCE: HUMAN NM
PUBLICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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GENERAL INFORMATION:
APPLICANT: KING, ET
TITLE OF INVENTION:
TITLE OF INVENTION:
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US-09-513-999C-5323
; Sequence 5323, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5323
; LUNCTH: 117
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Best Local Similarity 99.1%;
Matches 116; Conservative
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; ORGANISM: Homo sapiens
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/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-199-842-3
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US-09-248-796A-18029
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US-09-551-974A-20
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Sequence 491, App Sequence 1, Appli	Sequence 1, Appli	Appl	823, Ap	Sequence 59, Appl	Appl	16, A	equence 91, App	91, App	equence 3639, A	45, A	oo, a	Sequence 1, Appli	1,	Appl	Sequence 22989, A	σ
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US-09-538-092-491 US-08-713-825-1	09-199-8	US-09-460-532-1	8-092-8	US-09-443-184-59	US-10-227-035-4	9-1	US-09-358-972-91	US-09-790-417-91	9-583-110-363	9-107-433-3	US-09-107-532A-600(US-09-937-296-1	US-09-902-540-1038	US-09-937-296-2	ð	US-09-328-352-7960
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ALIGNMENTS

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0
US-09-335-948-5

Sequence 5, Application US/09335948

Patent No. 6329198

GENERAL INFORMATION:

APPLICANT: National Institutes of Health
APPLICANT: Charles R. King
APPLICANT: Lance A. Liotta

TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN

TITLE OF INVENTION: AND ANTIBODIES THEREFOR

FILE REFERENCE: 14014.0321

CURRENT APPLICATION NUMBER: US/09/335,948

CURRENT PILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 08/475,634

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1991-12-11

PRIOR FILING DATE: 1991-12-11

PRIOR FILING DATE: 1999-10-18

NUMBER OF SEQ ID NOS: 6

SOUTHWENT APPLICATION NUMBER: 07/422,801

PRIOR FILING DATE: 1989-10-18

NUMBER OF SEQ ID NOS: 6

SOUTHWENT APPLICATION NUMBER: 07/422,801

PRIOR FILING DATE: 1989-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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Pred. No. 2.4e-85;
Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-07-806-932B-1
; Sequence 1, Application US/07806932B
; Patent No. 6423836
; GENERAL INFORMATION:
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il Similarity 91.5%;
150; Conservative
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SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 150
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ORGANISM:
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               PRODUCTION AND USE OF HUMAN
HUMAN NM23 PROTEIN AND ANTIBODIES
THEREFOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 794; DB 2;
Pred. No. 2.4e-85;
1; Mismatches 10
                                                                                      : CARELLA, BYRNE, BAIN, GILFILLAN, S: CECCHI & STEWART 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-08-713-825-4
; Sequence 4, Application US/08713825
; Patent No. 5874285
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PR(
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/806,932B
FILING DATE: 11 december 1991
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,801
FILING DATE: 18 october 1989
ATTORNEY/AGENT INFORMATION:
NAME: CAPELLO, SUSAN A.
REGISTRATION NUMBER: 34,560
REFERENCE/DOCKET NUMBER: 469200-72
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1704
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 AMINO ACID RESIDUES
TYPE: AMINO ACID
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
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larity 91.5%;
Conservative
                                                                                                                                                                                                                                           PC-DOS
                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-D
SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICANT: KING, ET AL.
TITLE OF INVENTION: PROI
TITLE OF INVENTION: THEF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE: HUMAN PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN
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150; Conser
                                                                                                                                 CITY: ROSELAND
STATE: NEW JER
                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                        ADDRESSEE:
ADDRESSEE:
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                                                                                                                                                               COUNTRY:
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Best Local
Matches 15
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Phillip R.
NOVEL HUMAN NM23-LIKE PROTEIN
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Pred. No. 2.4e-81
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09199842;
Patent No. 6087125;
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
Incyte Pharmaceuticals, 4 Porter Drive
                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                      FILING DATE: Filed Herewith PRIOR APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.6%;
nilarity 94.1%;
Conservative
                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Diskette
IBM Compatible
SYSTEM: DOS
                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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MEDIUM TYPE: Diskett
COMPUTER: IBM COMPATING SYSTEM: DO
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468542
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              F: 3174 Por
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Best Local Similarity
Matches 143; Conser
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ADDRESSEE:
STREET: 3
CITY: Pal
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
US-08-713-825-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-199-842-4
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166
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FILING DATE: <Unknown>
APPLICATION NUMBER: 08/713,825
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acids
TYPE: amino acids
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 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/46
FILING DATE: 13-Dec-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: US-09-460-532-4
 3;
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ilarity 94.1%;
Conservative
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TOPOLOGY: linear
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COMPUTER READABLE FORM:
 Conservative
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143;
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US-09-460-532-4
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Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 759; DB 2; 1
Pred. No. 2.4e-81;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         759; DB 2;
No. 2.4e-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/335,948
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/475,634
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/806,932
PRIOR FILING DATE: 1991-12-11
PRIOR APPLICATION NUMBER: 07/422,801
PRIOR FILING DATE: 1989-10-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: National Institutes of Health APPLICANT: Charles R. King APPLICANT: Patricia S. Steeg APPLICANT: Lance A. Liotta TITLE OF INVENTION: PRODUCTION AND USE OF TITLE OF INVENTION: AND ANTIBODIES THEREFILE REFERENCE: 14014.0321
                                                                                                                      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                US/09/199,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score Pred. 1
                                                                           08/713,825
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Patent No. 6329198
GENERAL INFORMATION:
  FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
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94.1%;
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Best Local Similarity 94.1%;
Matches 143; Conservative
                                                                       APPLICATION NUMBER: 08/7
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              152 amino acids amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
               CURRENT APPLICATION DATA APPLICATION NUMBER: UFILING DATE:
                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                               single
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TYPE: PRT
ORGANISM: Homo Sapiens
IS-09-335-948-4
                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
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  SOFTWARE
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US-09-335-948-4
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                                                                                                   MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
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                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09460532

Patent No. 6486300

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
Hawkins, Phillip R.

TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTINGBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive

CITY: Palo Alto
STATE: CA
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Pred. No. 2.4e-81
}; Mismatches
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us-10-074-694

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NEW JERSEY
    FastSEQ for
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                                                                      ; ORGANISM: Homo US-09-335-948-2
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CITY: RO
STATE: N
COUNTRY:
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US-07-806-932B-3
                                  H: 176
PRT
   SOFTWARE: F
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Best Local
Matches 13
                                     LENGTH:
TYPE: PF
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FAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
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                                                                                                                                                                                                                                                                 Same
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APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Sam
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
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Patent No. 6329198
GENERAL INFORMATION:
APPLICANT: National Institutes of Health
APPLICANT: Charles R. King
APPLICANT: Patricia S. Steeg
APPLICANT: Lance A. Liotta
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature; LOCATION: (0)...(0); COCATION: (0)...(0); OTHER INFORMATION: Polypeptide Accession Number P15531US-09-538-092-933
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Pred. No. 2.4e-81;
3; Mismatches 6;
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                                                                      121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
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                                                       DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE
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CURRENT APPLICATION NUMBER: US/09/335,948
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/475,634
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/806,932
                                                                                                                                                                          Sequence 933, Application US/09538092
Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1991-12-11
PRIOR APPLICATION NUMBER: 07/422,801
PRIOR FILING DATE: 1989-10-18
NUMBER OF SEQ ID NOS: 6
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est Local Similarity 94.1%;
atches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                           US-09-538-092-933
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US-09-335-948-2
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                                                                                                                    Length 176;
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Pred. No. 2.7e-78
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/07806932B
; Patent No. 6423836
; GENERAL INFORMATION:
; TITLE OF INVENTION: PRODUCTION AND USE OF
; TITLE OF INVENTION: THEREFOR
; TITLE OF INVENTION: THEREFOR
; TITLE OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CECCHI & STEWART
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; CITY: NEW TENCEY
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11 december 1991
N: 530
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R: 469200-72
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FILING DATE: 11 december ...
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,801
FILING DATE: 18 october 1989
ATTORNEY/AGENT INFORMATION:
NAME: CAPELLO, SUSAN A.
REGISTRATION NUMBER: 34,560
REFERENCE/DOCKET NUMBER: 469200-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESIDUES
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: HUMAN NM 23-H2S
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
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Windows
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11 Similarity 90.2%;
138; Conservative
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AMINO ACIDS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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CURRENT APPLICATION DATA
APPLICATION NUMBER: U
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/199,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                          08/713,82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9;
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version CURRENT APPLICATION DATA:
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illarity 90.1%;
Conservative
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FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
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CLONE: 127983
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Best Local Similarity
Matches 137; Conser
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US-09-199-842-5
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                                                                                                                                               84 FFPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHG
                                                                                                                                 74 FFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHG
                                                                            14 TMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRP
                                                                                          24 TMANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRP
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Phillip R.
NOVEL HUMAN NM23-LIKE PROTEIN
         Score 734; DB 2; Le
Pred. No. 2.7e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 729; DB 1;
Pred. No. 8.4e-78;
9; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                            Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,825
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                           Sequence 5, Application US/08713825
Patent No. 5874285
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
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ilarity 90.1%;
Conservative
                        83.8%;
90.2%;
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                                                    Conservative
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TITLE OF INVENTION: NON
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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137; Conser
                       Query Match
Best Local Similarity
Matches 138; Conser
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US-07-806-932B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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US-08-713-825-5
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Pred. No. 8.4e-78;
Mismatches
                                                                                                                                 US-09-199-842-5
; Sequence 5, Application US/09199842
; Patent No. 6087125
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PRC;
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
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US-09-538-092-987
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LENGTH: 152
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                                         APPLICANT: National Institutes of Health
APPLICANT: Charles R. King
APPLICANT: Charles R. King
APPLICANT: Lance A. Liotta
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
FILE REFERENCE: 14014.0321
CURRENT APPLICATION NUMBER: US/09/335,948
CURRENT FILING DATE: 1999-06-18
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1991-12-11
PRIOR FILING DATE: 1991-12-11
PRIOR FILING DATE: 1991-12-11
PRIOR FILING DATE: 1999-10-18
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APPLICANT: Bandman, Olga
Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
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Pred. No. 8.4e-78;
; Mismatches 6;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,532
FILING DATE: 13-Dec-1999
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/199,842
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/713,825
                                                                                                                                                                                                                                                                                SEQ ID NOS: 6
FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible SYSTEM: DOS
Sequence 1, Application US/09335948 Patent No. 6329198
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Sequence 5, Application US/09460532
Patent No. 6486300
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llarity 90.1%;
Conservative
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COMPUTER READABLE FORM:
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US-09-335-948-1
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OPERATING
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hes 137; Conser
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                  Patent No. 6329198 GENERAL INFORMATION:
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CITY: Pa
STATE: C
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APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
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OTHER INFORMATION: Polypeptide Accession Number P22392
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8.4e-78;
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No. 8.4e-78
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             NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                       ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ce 987, Application US/09538092
No. 6753314
                                                                                                                                                 LENGTH: 152 amino acids
TYPE: amino acid
INFORMATION:
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ilarity 90.1%;
Conservative
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90.1%;
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ULE TYPE: peptide
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CLONE: 127983
SEQUENCE DESCRIPTION:
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ATTORNEY/AGENT
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i Sequence 2, Application US/08667023

j Patent No. 5817783

j GENERAL INFORMATION:

i APPLICANT: Callabreta, Bruno

APPLICANT: Wartinez, Robert V.

TITLE OF INVENTION: METHODS OF USING THE SAME

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewic

STREET: One Liberty Place, 46th floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA
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1.4e-56;
les 17;
                                                                                    Score 547.5; I
Pred. No. 2.4e-
2; Mismatches
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,023
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: MBER: US 60/000,427
FILING DATE: 22-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1992
TELEFONMUNICATION INFORMATION:
TELEFAK: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
TOPOLOGY: LIGHT AND ACIDS
TOPOLOGY: LIGHT AND ACIDS
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

December 16, 2005, 16:31:58 ; Search time 140.528 Seconds (without alignments) 763.122 Million cell updates/86 Run on:

updates/sec

Title: Perfect score: Sequence:

(E 152 US-10-074-694-5 803 1 MANLERTFIAIKPDGVQRGL.......WFKPEELVDYKSCAHDWVY

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

2166443 seqs, 705528306 residues Searched:

0.5

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_05.80:*
1: uniprot_grot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10000	111111	22392 homo	Q6fhn3 homo sapien	Q5rfh3 pongo pygma	9804 rattus	Q01768 mus musculu	C.	5 gallus	18 canis fa	Q90380 columba liv	Q05982 rattus norv	P15532 mus musculu	Q5nc81 m expressed	ın	4	4 bos tau	9 canis	5531 homo	9 homo	rc56 pongc	า สมาย	homo	0 ictal	2 cavia po	P70011 xenopus lae	pq80	8xg5	13 brachyda	f5 brachyda	0	azk9 xenopus tr	P70010 xenopus lae
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Q68F17_XENLA NDK8_HUMAN NDK_GINCI Q804YO_ONCMY O57560_SALSA Q6PC37_BRARE Q7SXL4_BRARE Q7ZZQ7_OREMO NDKA_DROME NDKA_DROYA Q5NC80_MOUSE Q7QIX6_ANOGA	Q4T9N6_TETNG
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GO; GO: 0005524; F:ATP binding; NAS.
GO; GO: 0004550; F:nucleoside-diphosphate kinase activity; TAS.
GO; GO: 0003700; F:transcription factor activity; TAS.
GO; GO: 0008285; P:negative regulation of cell proliferation; TAS.
GO; GO: 00063142; P:nucleoside triphosphate biosynthesis; NAS.
GO; GO: 0006315; P:regulation of transcription, DNA-dependent; TAS.
InterPro; IPR012005; NDK.
InterPro; IPR012005; NDK.
Pfam; PF00334; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
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                                                                                                                                                                                                                                    MEDLINE=9636368; PubMed=8747457; DOI=10.1016/S0969-2126(01)00
Morera S., Lacombe M.-L., Xu Y., Lebras G., Janin J.;
"X-ray structure of human nucleoside diphosphate kinase B comp with GDP at 2-A resolution.";
Structure 3:1307-1314(1995).
-!- FUNCTION: Major role in the synthesis of nucleoside tripho other than ATP.
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                                                                                                                                                  ndola C.E., Backer J.M., Williams R.L
a human nucleoside diphosphate kinas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00562; NDK; 1.
PROSITE; PS00469; NDP_KINASES; 1.
3D-structure; Activator; Anti-oncogene; ATP-binding; Cell
Direct protein sequencing; DNA-binding; Kinase; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                          ADP
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: The N-terminus is blocked.
DISEASE: This protein is found in reduced amount high metastasic potential.
SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                       1- FUNCTION: Acts as a transcriptional activator of binds DNA nonspecifically (Ref.3).
1- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate nucleoside triphosphate.
1- COFACTOR: Magnesium (By similarity).
1- SUBUNIT: Hexamer of two different chains: A and 3 A3B3, A2B4, AB5, B6).
1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
1- PTM: The N-terminus is blocked.
                                                                                                                                                                                                                                                                                                                                                                         diphosphate
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                                                                                       U.S.A. 99:16899-16903 (2002)
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OGP; P22392; -.

Ensembl; ENSG0000121054; Homo sapiens.

HGNC; HGNC: 7850; NME2.

H-InvDB; HIX0013993; -.

Partome; P22392; -.
                                                                                                            MEDLINE=95387396; PubMed=7658474; Webb P.A., Perisic O., Mendola C F T
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-; mRNA.
L; -; mRNA.
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PDB; INSK; X-ray; L/N/O/R/T/U=1-152
PDB; INUE; X-ray; A/B/C/D/E/F=2-152
TRANSFAC; T00706; -.
                                                                                                                                                                                                                           ANGSTROMS)
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EMBL; M36981; AAA36369.1; -; mRNA
EMBL; L16785; AAA60228.1; -; mRNA
EMBL; BC002476; AAH02476.1; -; mRNA
                                                                                                                                                                                              251:574-587 (1995)
                                                                         sequences."
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                                                                                         Sci.
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                                                                                         Acad.
                                                                         and mouse cDNA
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Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                 Gaps
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Substrate ATP/NDP ribose.
Substrate ATP/NDP base.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP base.
Substrate ATP/NDP ribose.
Substrate GDP N2.
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  metabolism;
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Last annotation update)
c cells 2, protein (NM23B)
         Transcription;
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Pred. No. 4.6e-70
Mismatches 0
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Chordata; Craniata
Euarchontoglires;
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Homo sapiens (Human).
Eukaryota; Metazoa; C
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Halleck A.,
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TISSUE=Chondrosarcoma;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M., Joaden T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Touchman J.W., Schmutz J., Myers R.M.,

Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                             Rolfs A., Halleck A., Hines L., Eisenstei
l J., Moreira D., Kelley T., LaBaer J., Li
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Ensembl; ENSG0000121054; Homo sapiens.

G0; G0:0005524; F:ATP binding; IEA.

G0; G0:0016301; F:Kinase activity; IEA.

G0; G0:0016740; F:nucleoside-diphosphate kinase activity; IEA.

G0; G0:0016740; F:transferase activity; IEA.

G0; G0:0006241; P:CTP biosynthesis; IEA.

G0; G0:0006228; P:UTP biosynthesis; IEA.

G0; G0:0006228; P:UTP biosynthesis; IEA.
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NIH MGC Project;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
Shen B., Henze S.,
                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                databases
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                                                                              Kalnine N., Chen X., Rolfs A., Halleck A., Hines L.,
Koundinya M., Raphael J., Moreira D., Kelley T., LaBa
Phelan M., Farmer A.;
"Cloning of human full-length CDSs in BD Creator(TM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 4.6e-70;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; CR541718; CAG46519.1;
EMBL; BT007045; AAP35694.1;
EMBL; BC095458; AAH95458.1;
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InterPro; IPR012005; NDK-2
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152 AA; 17
                Korn B., Zuo D., Hu Submitted (JUN-2004)
                                                                                                                                               ector.";
ubmitted (MAY-2003)
                                                                NUCLEOTIDE SEQUENCE.
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 ., Kstrang
Zuo D., Hu
                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Best Local Similarity
Matches 152; Conser
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                                                                                                                                               vector.
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; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                   activity;
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                                                                 QSRFH3 PONPY PRELIMINARY; PRT; 152 AA. QSRFH3; 051-FEB-2005 (TrEMBLrel. 29, Created) 01-FEB-2005 (TrEMBLrel. 29, Last sequence update) 01-FEB-2005 (TrEMBLrel. 29, Last annotation update) Hypothetical protein DKFZp468E0516.
                                                                                                                                                                                                                                                                                           GO; GO: 0005524; F: ATP binding; IEA.
GO; GO: 0016301; F: kinase activity; IEA.
GO; GO: 0016301; F: kinase activity; IEA.
GO; GO: 0016740; F: ransferase activity; IEA.
GO; GO: 0006241; P: CTP biosynthesis; IEA.
GO; GO: 000628; P: UTP biosynthesis; IEA.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
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Pred. No. 2.8e-69;
Mismatches
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                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
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(Rel. 17, Last sequence update)
(Rel. 48, Last annotation updat diphosphate kinase B (EC 2.7.4.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLWFKPEELVDYKSCAHDWVYE
DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE
                                                                                                                                                                                                                                          Weil B.,
           Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Euarchontoglires;
                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                               Consortium;
J., Mewes H.W.,
S.;
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Hypothetical protein.
SEQUENCE 152 AA; 17300 MW;
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                                                                                                                                                                                                                                                                 the
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Best Local Similarity 98.7%;
Matches 150; Conservative
                                                                                                                                                                                                                                                    Han M., Wiemann S.;
Submitted (NOV-2004) to the
EMBL; CR857184; CAH89484.1;
SMR; Q5RFH3; 2-152.
                                                                                                                                                                                                                                                                                                                                                                                           PIRSF000735; NDK; 1.
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SM00562; NDK; 1
                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                        TaxID=9600;
                                                                                                                                                                                                                                German cDNA
r A., Lauber
                                                                                                                                                                                                                                                                                                                                                                                            PF00334;
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P19804;
01-FEB-1991
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13-SEP-2005
Nucleoside di
(P18).
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                                                                                                                                                                                                             NUCLEOTIDE
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Pfam; PFO(
PIRSF; PI
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 121
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SMART; S
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                                                  RESULT
QSRFH3_
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the NDP
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                        eleostomi;
Sciurognathi;
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TISSUE=Brain;

NIH - Mammalian Gene Collection (MGC) project;

Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Major role in the synthesis of nucleoside triphosphate other than ATP. The ATP gamma phosphate is transferred to the beta phosphate via a ping-pong mechanism, using a phosphorylate active-site intermediate.

-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.

-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.

-!- COFACTOR: Magnesium (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic and plasma membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                            ide
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                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE=92332552; PubMed=1321145;
Ishikawa N., Shimada N., Munakata Y., Watanabe K., Kimura N.;
"Isolation and characterization of a gene encoding rat nucleos
                              ; Vertebrata; Euteleosto
Glires; Rodentia; Sciuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a leuke
                                                                                                                                                                                                                                                  clone encoding rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate and the restrate 
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ATP-binding; Direct protein sequencing; Kinase; Magnesium; Metal-binding; Nucleotide metabolism; Nucleotide-binding; Phosphorylation; Transferase.
ACT_SITE 118 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic and plasma membrane PTM: The N-terminus is blocked. SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rat mast cells of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ioinformatics Institute. There are no its content is in no way modified and
                                                                                                                                                    NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE
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                                                                                                                                                                                                                             Watanabe
                                                                                                                                                                          STRAIN=Wistar;
MEDLINE=90368787; PubMed=2168422;
Kimura N., Shimada N., Nomura K., Watanabe
"Isolation and characterization of a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Euarchontoglires; (
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M55331; AAA41684.1; -; mRNA.
EMBL; M91597; AAA42017.1; -; mRNA.
EMBL; BC086599; AAH86599.1; -; mRNA.
PIR; A41849; A38369.
HSSP; P22392; 1NUE.
SMR; P19804; 2-152.
Ensembl; ENSRNOG0000002671; Rattus no RGD; 619877; Nme2.
InterPro; IPR012005; NDK.
InterPro; IPR012005; NDK-2.
Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley; TISSUE=Mast ce MEDLINE=92256389; PubMed=1316151; Hemmerich S., Yarden Y., Pecht I.; "A cromoglycate binding protein from is a nucleoside diphosphate kinase."; Biochemistry 31:4574-4579(1992).
                                                                                                                                                                                                                                                                        diphosphate kinase.";
nem. 265:15744-15749(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 diphosphate kinase.";
J. Biol. Chem. 267:14366-14372(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                   NCBI_TaxID=10116;
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

NUCLEOTINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

A Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Batic R., Suzuki H., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Faragin A., Matsuda H., Batalov S., Beisel K.W.,

Blake J.A., Brada D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Achai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kawaji H., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Nerardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I.,

Wilming L.G., Wanker A., Carminci P., Hayatsu N.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sakazume S.,

Shiraki T., Waki Y., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

Shiraki T., Waki Y., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
                                                                                                                                                                                    1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi
Muroidea; Muridae; Murinae; Mus.
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MEDLINE=92387389; PubMed=1325378; DOI=10.1016/0014-5793(92)80807-S;
Urano T., Takamiya K., Furukawa K., Shiku H.;
"Molecular cloning and functional expression of the second mouse nm23/NDP kinase gene, nm23-M2.";
FEBS Lett. 309:358-362(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NDP kinase
                                                                         ·;
                                    Length 152;
                                                                         Indels
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                                                                         1;
1A5C3F84C1F413EC
                                    3.5e-69;
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01-APR-1993 (Rel. 25, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Nucleoside diphosphate kinase B (EC 2.7.4.6)
(nm23-M2) (P18).
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                                                     ed. No. 3.5e
Mismatches
                                                                                                                                                                                                                                                                                DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE
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                                    Score 794;
Pred. No.
                                                                         7
17283 MW;
                                 98.9%;
illarity 98.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muroidea; Muridae
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                         NDKB MOUSE
Q01768;
01-APR-1993
01-APR-1993
                                                                        149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takeshi U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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                                     Query Match
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                                                                                                                       of
                                                                                                                                                                                                                               STRAIN=C57BL/6; TISSUE=Brain, and Heart;

KEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buuetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., More T., Max S.I., Wang J., Hsieh F.,

A piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human T and mouse cDNA semience "I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 th human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated active-site intermediate.

-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.

-!- COFACTOR: Magnesium (By similarity).

-!- COFACTOR: ASS, BS, BS).
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hy S.J.,
P.H.,
yk S.W.,
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Phosphorylation; Transferase.
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Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional anr 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s Swiss-Prot entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restras long as its content is in no way modified and this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and plasma membrane.
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MGI; MGI:97356; Nme2.
GO; GO:0005739; C:mitochondrion; IDA.
InterPro; IPR01564; NDK.
InterPro; IPR012005; NDK-2.
Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
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SUBCELLULAR LOCATION: Cytoplasmic and SIMILARITY: Belongs to the NDK family.
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mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE, PS00469; NDP ATP-binding; Kinase, No Nucleotide-binding; PhacT SITE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDK;
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                                                                  FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
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ia; Sciurognathi;
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                            Length 152
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004550; F:nucleoside-diphosphate kinase activity;
GO; GO:0006241; P:CTP biosynthesis; IEA.
GO; GO:0006183; P:GTP biosynthesis; IEA.
GO; GO:0006228; P:UTP biosynthesis; IEA.
InterPro; IPR01264; NDK.
InterPro; IPR012005; NDK-2.
Pfam; PF00334; NDK; 1.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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cells 2 protein.
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similarity).
1A5C3F84C1FFC83C
                           ore 793; DB 1;
red. No. 4.4e-69;
Mismatches 1
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Pred. No. 4.4e-69;
2; Mismatches
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3.1; -; Genomic_DNA.
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Pred.
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PKINASES; 1
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Q5NC82;
01-FEB-2005 (TrEMBLrel. 29, C;
01-FEB-2005 (TrEMBLrel. 29, L;
01-FEB-2005 (TrEMBLrel. 29, L;
Expressed in non-metastatic C;
ORFNames=RP23-378113.2-002;
Mus musculus (Mouse).
          17363 MW;
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                            98.8%;
ilarity 98.0%;
Conservative
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Best Local Similarity 98.0%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Mashreghi-Mohammadi M.;
Submitted (FEB-2005) to the
EMBL; AL662838; CAI35363.1;
SMR; Q5NC82; 2-152.
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SMART; SM00562; NDK
PROSITE; PS00469; NI
SEQUENCE 152 AA;
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149; Conser
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
O57535_CHICK
O57535_CHICK PRELIMINARY; PRT; 153 AA.
O57535;
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
F 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
F 01-JUN-1998 (TrEMBLrel. 25, Last annotation update)
Nucleoside diphosphate kinase.
Name=cNDPK;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianir
Gallus.
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF043542; AAB99856.1; -; mRNA.
HSSP; P22392; 1NUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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Last annotation update)
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No. 5.4e-65
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HSSP; P22392; 1NUE.
SMR; O57535; 3-153.

ENSembl; ENSGALG00000002932; Gallus gallus.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006241; P:CTP biosynthesis; IEA.
GO; GO:000628; P:UTP biosynthesis; IEA.
InterPro; IPR012005; NDK.
InterPro; IPR012005; NDK.
InterPro; IPR012005; NDK.
PRINTS; PR01243; NUCDPKINASE.
PRODOM; PD001018; NDK; 1.
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QSOKA8;
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
NMC3-C2.
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PROSITE; PS00469; NDP
                                                                                                                                                                                                                                                  SEQUENCE
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TISSUE=Liver
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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A madeth D.O., Mehus J.G., Ivey M.A., Milavetz B.I.;

Lambeth D.O., Mehus J.G., Ivey M.A., Milavetz B.I.;

"Characterization and cloning of a nucleoside-diphosphate kinase

T argeted to matrix of mitochondria in pigeon.";

J. Biol. Chem. 272:24604-24611(1997).

C -!- FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated active-site intermediate.

C -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.

C -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.

C -!- COFACTOR: Magnesium (By similarity).

C -!- SUBCELLULAR LOCATION: Cytoplasmic and plasma membrane.

C -!- SUBCELLULAR LOCATION: Cytoplasmic and plasma membrane.

C -!- SUBCELLULAR LOCATION: Cytoplasmic and blasma membrane.

C -!- SIMILARITY: Belongs to the NDK family.
                                                 expression in normal
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Craniata, Vertebrata, Euteleostomi;
; Columbiformes; Columbidae; Columba
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17366 MW; 923DA489B37C19C6
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 750; DB 2;
Pred. No. 6.7e-65;
); Mismatches 3
Fukushima K., Fujiki M.,
                                                                                                    the EMBL/GenBank/DDBJ
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15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Nucleoside diphosphate kinase (EC 2.7.4.6) (N
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       Takahashi M., Une K., Fukushiwa A., Endo Y., Oishi A., Akuzawa M.;
"Molecular cloning of canine nm23 cI and tumor tisuues.";
Submitted (MAR-2005) to the EMBL/Ger EMBL; AB207045; BAD97838.1; -; mRNA.SMR; Q50KA8; 2-152.
InterPro; IPR01264; NDK.
InterPro; IPR012005; NDK.
Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
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Eukaryota, Metazoa, Chordata, C
Archosauria, Aves, Neognathae,
NCBI_TaxID=8932;
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ilarity 92.1%;
Conservative
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152 AA; 1
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TISSUE=Liver;
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s transferred to the NDP
using a phosphorylated
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bition
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NUCLEOTIDE SEQUENCE.
MEDLINE=93155067; PubMed=8381409;
Shimada N., Ishikawa N., Munakata Y., Toda T., Watanabe K., Kimura N., Second form (beta isoform) of nucleoside diphosphate kinase from rat. Isolation and characterization of complementary and genomic DNA
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                                          Interrac,
Interpro; IPR012000,
Interpro; IPR0134; NDK; 1.
R PIRSF000735; NDK; 1.
R PRINTS; PR01243; NUCDFKINASE.
R PRODOM; PD001018; NDK; 1.
R PROSITE; PS00469; NDP KINASES; 1.
RPOSITE; PS00469; NDP KINASES; 1.
RATP-binding; Kinase; Magnesium; Metal-binding; Nucleotide metaboli (W Nucleotide-binding; Phosphorylation; Transferase.

Nucleotide-binding; Phosphorylation; Transferase.

Nucleotide-binding; Phosphorylation; Transferase.

Nucleotide-binding; Phosphorylation; Transferase.

Nucleotide-binding; Phosphorylation; Transferase.

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Nucleotide-binding; Phosphorylation; Transferase.

Nucleotide-binding; Phosphorylation; Transferase.

Nucleotide-binding; Phosphorylation; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and expression.";

J. Biol. Chem. 268:2583-2589(1993).

-!- FUNCTION: Major role in the synthesis of nucleoside triphosy other than ATP. The ATP gamma phosphate is transferred to the phosphate via a ping-pong mechanism, using a phosphorylactive-site intermediate.

-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.

-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.

-!- COFACTOR: Magnesium (By similarity).

-!- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A3B3, A2B4, AB5, B6). Interacts with SET (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

-!- DISEASE: This protein is found in reduced amount in tumor of high metastasic potential.

-!- SIMILARITY: Belongs to the NDK family.
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Glires; Rodentia;
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                                                                                                                                                                                                                    Score 744; DB 1; Le
Pred. No. 2.6e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   005982;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside diphosphate kinase A (EC 2.7.4.6)
(Tumor metastatic process-associated protein)
factor NM23).
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    Genomic DNA
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Mammalia; Eutheria; Euarchontoglires; (
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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    AAC78437.1;
                                                                                                                                                                                                                                              137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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EMBL; AF018266; AAC784
HSSP; P22392; INUE.
SMR; Q90380; 3-153.
InterPro; IPR001564; N
InterPro; IPR012005; N
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HSSP; P15531; LU...
HSSP; P15531; LU...
RSMR; Q05982; 5-152.
REBSEMbl; ENSRNOG000002693; Rattus ILL...
RGD; 70497; Nme1.
RGD; 70497; Nme1.
RGD; G0:0005813; C:Centrosome; IDA.
RGD; G0:0005813; C:Centrosome; IDA.
RICHEPPO; IPR012005; NDK-2.
DR InterPro; IPR012005; NDK-2.
DR PRINTS; PR01243; NUCDPKINASE.
DR PRINTS; PR01243; NUCDPKINASE.
DR RMART; SM00562; NDK; 1.
DR SMART; SM00562; NDK; 1.
DR RNOSITE; PS00469; NDP KINASES; 1.
DR RTP-binding; Kinase; Magnesium; Metal-binding; Nucleotide-binding; Phosphorylation; Transferase.
Nucleotide-binding; Phosphorylation; Transferase.
Nucleotide-binding; Phosphorylation; Transferase.
Art SITE 118 118 Pros-phosphohistidine intermediate (By similarity).
THE SITE 118 118 Pros-phosphohistidine intermediate (By similarity).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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restrictions (this statement
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MEDLINE=88155671; PubMed=3346912;
Steeg P.S., Bevilacqua G., Kopper L., Thorgeirsson U.P.,
Talmadge J.E., Liotta L.A., Sobel M.E.;
"Evidence for a novel gene associated with low tumor metastatic potential.";
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MEDLINE=90044071; PubMed=2509941; DOI=10.1038/342177a0;
Rosengard A.M., Krutzsch H.C., Shearn A., Biggs J.R., Barker
Margulies I.M.K., King C.R., Liotta L.A., Steeg P.S.;
"Reduced Nm23/Awd protein in tumour metastasis and aberrant I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
      There are no modified and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 732; DB 1; 1
Pred. No. 3.8e-63;
); Mismatches 5;
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01-APR-1990 (Rel. 14, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside diphosphate kinase A (EC 2.7.4.6)
(Tumor metastatic process-associated protein)
factor NM23) (NDPK-A) (nm23-M1).
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il Similarity 90.1%;
137; Conservative 1
                                                                                                                                              EMBL; D13374; BAA02635.1;
PIR; A45208; A45208.
HSSP; P15531; 1JXV.
SMR; Q05982; 5-152.
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Mus musculus (Mouse).
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the NDP
rylated
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STRAIN=FVB/N; TISSUE=Mammary gland;

KETAIN=FVB/N; TISSUE=Mammary gland;

KITAIN=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KITAIN=STRAIN=FVB/N; TISSUE=Mammary gland;

KITAIN=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KITAIN=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KITAIN=EXECTAIN F.S., Manner E.A., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wanner C.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Kichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Kahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez B.C., Grimples S.J.M., Mara M.J.,

Rodriguez B.C., Schmutz J.M., Mara M.J.,

Rodriguez B.C., Schmutz J.M.,

Rodrigu
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Ν. Σ.
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K.,
                                                                                 04-M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Major role in the synthesis of nucleoside triphosy other than ATP. The ATP gamma phosphate is transferred to the beta phosphate via a ping-pong mechanism, using a phosphoryly active-site intermediate.

-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.

-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.

-!- COFACTOR: Magnesium (By similarity).

-!- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A3B3, A2B4, AB5, B6). Interacts with SET (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

-!- DISEASE: This protein is found in reduced amount in tumor of high metastasic potential.

-!- SIMILARITY: Belongs to the NDK family.
                                                                      MEDLINE=91191558; PubMed=2013093; DOI=10.1016/0092-8674(91)904 Leone A., Flatow U., King C.R., Sandeen M.A., Margulies I.M., Liotta L.A., Steeg P.S.; "Reduced tumor incidence, metastatic potential, and cytokine responsiveness of nm23-transfected melanoma cells."; Cell 65:25-35(1991).
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is transferred to
n, using a phosphor
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EMBL
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                                                                                                                                                                                                                                                                                                                  Daniel J.Y.; the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                    i M., Lombardi D.;
to the EMBL/GenBank/DDBJ databases
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PAGE; P15532; MOUSE.
ENSMUSG00000037601; Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M35970; AAA39826.1; ALT_INIT; mRNA.
EMBL; M65037; AAA63391.1; -; mRNA.
EMBL; U85511; AAB42080.1; -; mRNA.
EMBL; AF033377; AAB87689.1; -; mRNA.
EMBL; BC005629; AAH05629.1; -; mRNA.
PIR; A46557; A46557.
HSSP; P15531; 1JXV.
  80:200-204(1988)
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Gervasi F., Fanciulli M., L
Submitted (NOV-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   long as its content
                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
STRAIN=129/Sv;
Dabernat S., Masse K., D
Submitted (FEB-1997) to
Inst.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                     NUCLEOTIDE SEQUENCE
  Cancer
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S-2DPAGE;
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SWISS-2DP
Ensembl;
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), full insert
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Expressed in non-metastatic cells 1 protein (12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430059B17 product:expressed in non-metastatic cells 1, protein (NM23A) (nucleoside diphosphate kinase), full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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STRAIN=C57BL/6J;
TISSUE=Embryonic body between diaphragm region and neck;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
MGI; MGI:97355; Nmel.

GO; GO:0005792; C:microsome; IDA.

GO; GO:0005625; C:soluble fraction; IDA.

InterPro; IPR001564; NDK.

InterPro; IPR012005; NDK-2.

Pfam; PF00334; NDK; 1.

PIRSF; PR01243; NUCDPKINASE.

PRODOm; PD001018; NDK; 1.

R ProDom; PD001018; NDK; 1.

R ProDom; PS00469; NDK; 1.

R PROSITE; PS00469; NDP KINASES; 1.

RATP-binding; Kinase; Magnesium; Metal-binding; Nucleotide metabolism; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                  152
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EE2E4DB218024686 CR
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Pred. No. 7.5e-63;
9; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                   118 P. 17208 MW;
                                                                                                                                                                                                                                                                                                                                                                                 90.8%;
ilarity 90.1%;
Conservative
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QSNC81;
01-FEB-2005 (TrEMBLrel. 29,
01-FEB-2005 (TrEMBLrel. 29,
10-MAY-2005 (TrEMBLrel. 30,
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Mashreghi-Mohammadi Submitted (FEB-2005)
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STRAIN=CSTBL/6J;

C TISSUE=Embryonic body between diaphragm region and neck;

TISSUE=Embryonic body between diaphragm region and neck;

TISSUE=Embryonic body between diaphragm region and neck;

NEDLINE=2254683; PubMed=12466851; DOI=10.1038/natureol1266;

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Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

A vagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,

Baldarelli R., Hill D.P., Bulf C., Hume D.A., Quackenbush J.,

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I Nature 420:563-573(2002).
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Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw.
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TISSUE=Embryonic body between diaphragm region and neck;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh Numami N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada Pyamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
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STRAIN=C57BL/6J;

TISSUE=Embryonic body between diaphragm region and neck;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

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                                                                                                                                                                                                                                                                                                                                  a full-length mouse cDNA collection
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A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

A Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

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Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T.,

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Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

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E Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

B SMR; QSNC81; 5-152.

R GO; GO:0005524; F:ATP binding, IEA.

GO; GO:0006528; F:ATP binding, IEA.

GO; GO:0006228; F:ATP binding, IEA.

GO; GO:0006228; F:UTP biosynthesis; IEA.

GO; GO:0006228; P:UTP biosynthesis; IEA.

InterPro; IPR012005; NDK-2.

P Fam: PP001314. NDW.
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SUBCELLULAR LOCATION, BLOCKAGE OF THE N-TERMINUS, AND X-RAY
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15-JUL-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Nucleoside diphosphate kinase NBR-B (EC 2.7.4.6) (NDF kinase NBR-B).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Bovidae; Bovinae; Bos.
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Pred. No. 7.5e-63
); Mismatches
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pipeline with 384 multicapillary 10:1757-1771 (2000).
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PDB; 1BE4; X-ray; A/B/C=1-151.

InterPro; IPR001564; NDK.

InterPro; IPR012005; NDK-2.

Pfam; PF00334; NDK; 1.

PIRSF; PRO1243; NUCDPKINASE.

ProDom; PD001018; NDK; 1.

SMART; SM00562; NDK; 1.

SMART; SM00562; NDF; 1.

RAGNESITE; PS00469; NDP KINASES; 1.

RAGNESIUM; Metal-binding; Direct protein sequencing; Kinase; Nucleotide-binding; Phosphorylation; Transferase.

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CRYSTALLOGRAPHY (2.4 ANGSTROMS).

TISSUE=Retina;

MEDLINE=98434367; PubMed=9760230; DOI=10.1021/bi9808538;

Abdulaev N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L.,

Yakhyaev A.V., Tordova M., Gaidarov I.O., Popov V.I., Fujiwara
Chinchilla D., Eisenstein E., Gilliland G.L., Ridge K.D.;

"Nucleoside diphosphate kinase from bovine retina: purification
subcellular localization, molecular cloning, and three-dimensi
                                                                                       nucleoside triphosphate.
COFACTOR: Magnesium (By Similarity).
SUBUNIT: Homohexamer.
SUBCELLULAR LOCATION: Cytoplasmic and localized to the pla
                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
use as long as its content is in no way modified and this stat
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Biochemistry 37:13958-13967(1998).
-!- FUNCTION: Major role in the synthesis
   other than ATP.
-!- CATALYTIC ACTIVITY: ATP + nucleoside c
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Biochemistry 37:13958-13967(1998).
-! - FUNCTION: Major role in the synthesis of nucleoside triphosphates
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MEDLINE=98434367; PubMed=9760230; DOI=10.1021/bi980853s;
Abdulaev N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L.,
Yakhyaev A.V., Tordova M., Gaidarov I.O., Popov V.I., Fujiwara J.H
Chinchilla D., Eisenstein E., Gilliland G.L., Ridge K.D.;
"Nucleoside diphosphate kinase from bovine retina: purification, subcellular localization, molecular cloning, and three-dimensional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleoside triphosphate.
COFACTOR: Magnesium (By similarity).
SUBUNIT: Homohexamer.
SUBCELLULAR LOCATION: Cytoplasmic and localized to the
                                                                                    Length 151;
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Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Pecora; Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other than ATP. CATALYTIC ACTIVITY: ATP + nucleoside diphosphate
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                                          AACDC542C77864E1
                                                                                   ore 728; DB 1;
ed. No. 9.3e-63;
Mismatches 4
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to the NDK family
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(Rel. 38, Last sequence un
(Rel. 47, Last annotation
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PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE
ProDom; PD001018; NDK; 1.
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15-JUL-1999
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NCBI_TaxID=9913;
[1]
NUCLEOTIDE SEQUENCE.
TISSUE=Lymphoid;
                                         Bm;
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                                                                            Pros-phosphohistidine intermediate
Substrate ATP/NDP ribose.
Substrate ATP/NDP base.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP base.
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PROSITE; PS00469; NDP KINASES; 1.

3D-structure; ATP-binding; Direct protein sequencing; Magnesium; Metal-binding; Nuclear protein; Nucleotide Nucleotide-binding; Phosphorylation; Transferase.

INIT MET 0 0 0 ACT SITE 117 117 Pros-phosphohistidine int
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10-MAY-2005 (TrEMBLrel. 30,
10-MAY-2005 (TrEMBLrel. 30,
NDP kinase NBR-A.
Bos taurus (Bovine).
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Yu J., Meng Y., Wang Z., Hansen C., Li C., Moore S.;

"Analysis of sequences obtained from constructed full-length bovine cDNA libraries.";

Lubmitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; AY911378; AAW82141.1; -; mRNA.

EMBL; AY911378; AAW82141.1; -; mRNA.

EMBL; AY911378; AAW82141.1; -; mRNA.

RO; GO:000524; F:ATP binding; IEA.

GO; GO:000524; F:ATP binding; IEA.

GO; GO:0006241; P:Kinase activity; IEA.

GO; GO:0006241; P:CTP biosynthesis; IEA.

GO; GO:0006241; P:CTP biosynthesis; IEA.

GO; GO:000628; P:UTP biosynthesis; IEA.

RO; GO:000628; P:UTP biosynthesis; IEA.

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R FAM; PF00334; NDK; 1.

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es/sec ; Search time 153.472 Sec (without alignments) 763.122 Million cell updat

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US-10-074-694-3 Title:

QSQPAVKPCHLKGTMANSER 876 score: Sequence: Perfect

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705528306 residues 2166443 seqs, Searched:

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UniProt_05.80:*
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a inted, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.

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STRAIN=FVB/N; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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STRAIN=Swiss Webster / NIH;
Gervasi F., Fanciulli M., Lombardi D.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside diphosphate kinase A (EC 2.7.4.6)
(Tumor metastatic process-associated protein)
factor NM23) (NDPK-A) (nm23-M1).
Name=Nmel; Synonyms=Nm23;
Mus musculus (Mouse).
                            Æ
                           152
                          PRT;
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Euarchontog
Muroidea; Muridae; Murinae; Mus
NCBI TaxID=10090;
                            STANDARD;
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Cell 65:25-35(1991)
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                            NDKA MOUSE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated extive-site intermediate.

-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.

-!- COFACTOR: Magnesium (By similarity).

-!- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2, A3B3, A2B4, AB5, B6). Interacts with SET (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

-!- SUBCELLULAR beto protein is found in reduced amount in tumor cells of high metastasic potential.

-!- SIMILARITY: Belongs to the NDK family.
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B.W.,
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length hum
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D.,
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CRC64;
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ATP-binding; Kinase; Magnesium; Metal-binding; Nuclear protein;
Nucleotide metabolism; Nucleotide-binding; Phosphorylation;
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Pred. No. 6.5e-67;
0; Mismatches 0;
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GO; GO:0005792; C:microsome; IDA.
GO; GO:0005625; C:soluble fraction; IDA.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
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EMBL; M65037; AAA63391.1; -; mRNA.
EMBL; U85511; AAB42080.1; -; mRNA.
EMBL; AF033377; AAB87689.1; -; mRNA.
EMBL; BC005629; AAH05629.1; -; mRNA.
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100.0%;
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PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P15531; 1JXV.
SMR; P15532; 5-152.
SWTSS-2DPAGE; P15532; MOUSE.
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NUCLECTIDE SEQUENCE.

STRAIN=C57BL/6J;

C TISSUE=Embryonic body between diaphragm region and neck;

X MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

X Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wasner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Autonis H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                   OSNC81;
OSNC81;
OSNC81;
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Expressed in non-metastatic cells 1 protein (12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430059B17 product:expressed in non-metastatic enriched library, clone:9430059B17 product:expressed in non-metastatic enriched library, clone:9430059B17 product:expressed in non-metastatic enriched library, clone:9430059B17 product:expressed in non-metastatic
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Embryonic body between diaphragm region and neck;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9,
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Embryonic body between diaphragm region and neck;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA collection.";
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Submitted (FEB-2005)
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STRAIN=C57BL/6J;
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"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Walls C., Wang Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Yang Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Chillan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Chillan R., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Chillan R., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Chillan R., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Chillan R., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Chillan R., Carninci P., Hayatsu N., Chillan R., Carninci P., Rama Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Chillan R., Carninci P., Rama Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Chillan R., Carninci P., Rama Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Rama Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Rama Z., Zavolan M., Zhu Y., Zimmer R., Carninci P., Rama Z., Zavolan M., Carninci P., 
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Nokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryonic body between diaphragm region and neck;
A dachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Ako34899; BAC28873.1; -; MRNA.
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TISSUE=Embryonic body between diaphragm region and neck;
TISSUE=Embryonic body between diaphragm region and neck;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new ge Genome Res. 10:1617-1630(2000).
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NUCLECTIDE SEQUENCE.

TISSUE=Eye;

KEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KETAUSDEEY R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M.J., Usdin T.B., Bonaldo M.F., Carainci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                     FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi
Muroidea; Muridae; Murinae; Mus.
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0
                                                                                                                                                                                                                                               Length 152;
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                                                                                                                                                                                                                 EE2E4DB218024686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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0
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Pred. No. 6.5e-67;
); Mismatches 0;
                kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 AA
                              IEA
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0004550; F:nucleoside-diphosphate ki
GO; GO:0016740; F:transferase activity; IEA
GO; GO:0006241; P:CTP biosynthesis; IEA.
GO; GO:0006183; P:GTP biosynthesis; IEA.
GO; GO:0006228; P:UTP biosynthesis; IEA.
InterPro; IPR001564; NDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                   PF00334; NDK; 1.; PIRSF000735; NDK; 1.
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Q80VT7;
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Mus musculus (Mouse).
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PROSITE; PS00469; NDP
                                                                                                                                                                     NDK;
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152; Conser
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NCBI_TaxID=10090;
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01-JUN-2003
01-OCT-2003
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Pfam; PFO(
PIRSF; PI
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Best Local S
Matches 152
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NUCLEOTIDE SEQUENCE TISSUE=Eye;

Ensembl; ENSMUSG0000037601; Mus mi GO; GO:0005524; F:ATP binding; IEA

Q5NC81;

SMR;

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Homo.
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Matches
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CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
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NUCLEOTIDE SEQUENCE.
MEDLINE=93155067; PubMed=8381409;
Shimada N., Ishikawa N., Munakata Y., Toda T., Watanabe K., Kimu:
"A second form (beta isoform) of nucleoside diphosphate kinase form the second form (beta isoform) of second diphosphate kinase form the second form (beta isoform) of second diphosphate kinase form the second form (beta isoform) of second diphosphate kinase form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the second form the secon
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogn
Muroidea; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
NIH MGC Project;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ATP + nucleoside.diphosphate = ADP +
nucleoside triphosphate.

-!- SIMILARITY: Belongs to the NDK family.

EMBL; BC027044; AAH27044.2; -; mRNA.
HSSP; P15531; 1JXV.

SMR; Q80VT7; 28-176.

Ensembl; ENSMUSG00000037601; Mus musculus.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006550; F:nucleoside-diphosphate kinase activity; IEA.
GO; GO:0006281; P:CTP biosynthesis; IEA.
GO; GO:0006281; P:CTP biosynthesis; IEA.
GO; GO:0006282; P:UTP biosynthesis; IEA.
GO; GO:0006283; P:UTP biosynthesis; IEA.
InterPro; IPR001564; NDK.
PFam; PF00334; NDK.
                                                                      +
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No. 1.8e-66;
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01-FEB-1994 (Rel. 28, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside diphosphate kinase A (EC 2.7.4.6)
(Tumor metastatic process-associated protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00469; NDP_KINASES; 1.
ATP-binding; Kinase; Nucleotide-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268:2583-2589(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.6%;
91.5%;
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S; PR01243; NUC
m; PD001018; ND
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Biol. Chem. 2
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                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use as long as its content is in no way modified and this statement is no
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Primates; Catarrhini; Hominidae
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                                                           cells
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PROSITE; PS00469; NDP_KINASES; 1.
ATP-binding; Kinase; Magnesium; Metal-binding; Nucleotide metabo
Nucleotide-binding; Phosphorylation; Transferase.
Nucleotide-binding; Phosphorylation; Transferase.
ACT_SITE 118 Pros-phosphohistidine intermediate similarity).
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152;
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MEDLINE=22489419; PubMed=12601555; DOI=1
Ni X., Gu S., Dai J., Cheng H., Guo L.,
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Euarchontoglires; P.
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"Isolation and characterization of
different transcript of NM23-H1.";
                                                                                                                                                                                             EMBL; D13374; BAA02635.1; -; mRNA
PIR; A45208; A45208.
                                                                                                                                                                                                                                                                                GO; GO:0005813; C:centrosome; IDA InterPro; IPR001564; NDK. InterPro; IPR012005; NDK-2. Pfam; PF00334; NDK; 1.
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illarity 96.7%;
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PRINTS; PR01243; NUCDPKINASE
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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147; Conserv
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Ghosh L., c
              Wang L., Patel U., Ghosh L. "Mutation in the nm23 gene
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Proteins 46:340-342(2002)
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                                                                                                                                  SEQUENCE
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                                                                                    Cancer Res.
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MEDLINE=90044071; PubMed=2509941; DOI=10.1038/342177a0;
Rosengard A.M., Krutzsch H.C., Shearn A., Biggs J.R., Barker E., Margulies I.M.K., King C.R., Liotta L.A., Steeg P.S.; "Reduced Nm23/Awd protein in tumour metastasis and aberrant Dros development.";
Nature 342:177-180(1989).
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asis inhibi
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homi
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MEDLINE=94095204; PubMed=8270257; DOI=10.1007/BF00218915;
Dooley S., Seib T., Engel M., Theisinger B., Janz H., Piontek K.
Zang K.D., Welter C.;
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                                                                                                                                                        activity;
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01-APR-1990 (Rel. 14, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A)
(Tumor metastatic process-associated protein) (Metasfactor nm23) (nm23-H1) (Granzyme A-activated DNase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 774.5; DB 2;
Pred. No. 1.3e-64;
4; Mismatches 11;
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IEA.
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                                              Ensembl; ENSG0000011052; Homo sapiens.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016301; F:Kinase activity; IEA.
GO; GO:0016740; F:Rucleoside-diphosphate ki
GO; GO:0016740; F:Rucleoside-diphosphate ki
GO; GO:0006241; P:CTP biosynthesis; IEA.
GO; GO:0006183; P:GTP biosynthesis; IEA.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
Pfam; PF00334: NDK.
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MEDLINE=93153759; PubMed=7916650;
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Homo sapiens (Human).
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the putative metastasis control
Hum. Genet. 93:63-66(1994).
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                                                                                                                                                                                                                                                                                                                                                                    NUCDPKINASE
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90.2%;
                 EMBL; AF487339; AA085436.1;
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PRINTS; PR01243; NUCDPI
ProDom; PD001018; NDK;
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                                          531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are associated with
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MEDLINE=22515524; PubMed=12628186; DOI=10.1016/S0092-8674(03)00150-8;
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MEDLINE=91224972; PubMed=1851158;
Gilles A.-M., Presecan E., Vonica A., Lascu I.;
"Nucleoside diphosphate kinase from human erythrocytes. Structural characterization of the two polypeptide chains responsible for heterogeneity of the hexameric enzyme.";
J. Biol. Chem. 266:8784-8789(1991).
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Aontbrun S., Schneider B., Veron M., Morera S.,
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MEDLINE=91277302; PubMed=2056128;
Hailat N., Keim D.R., Melhem R.F., Zhu X.X., Eckerskorn C.,
Brodeur G.M., Reynolds C.P., Seeger R.C., Lottspeich F.,
Strahler J.R., Hanash S.J.;
"High levels of p19/nm23 protein in neuroblastoma are associadvanced stage disease and with N-myc gene amplification.";
J. Clin. Invest. 88:341-345(1991).
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MEDLINE=21824372; PubMed=11835509; DOI=10.1002/prot.10038;
Min K., Song H.K., Chang C., Kim S.Y., Lee K.J., Suh S.W.;
"Crystal structure of human nucleoside diphosphate kinase metastasis suppressor.":
Chen H.C., Banerjee S.; sassociated with metastasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
[5]
                                                                                                                                         [LARGE SCALE MRNA]
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through a collaboration at the EMBL outstation - no restrictions on its
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13
                                                                                                                                                                                                                           other than ATP.

-1- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
nucleoside triphosphate.
-1- COFACTOR: Magnesium.
-1- COFACTOR: Magnesium.
-1- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2, A3B3, A2B4, AB5, B6). Interacts with SET.
-1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
-1- TISSUE SPECIFICITY: Expressed in lung carcinoma cell lines but not in normal lung tissues.
-1- FTM: The N-terminus is blocked.
-1- DISEASE: This protein is found in reduced amount in tumor cells of high metastasic potential. Somatic mutations of NME1 are found in neuroblastoma. Increased NME1 in neuroblastoma is correlated with features of the disease that are associated with aggressive tumors. May therefore have distinct if not opposite roles in
                                                                                                                                                                                                                                                                                                                                                             ut not
                                                                                                  VARIANT NEUROBLASTOMA GLY-120.

MEDLINE=94322908; PubMed=8047138; DOI=10.1038/370335a0;
Chang C.L., Zhu X.-X., Thoraval D.H., Ungar D., Rawwas J., Hora N., Strahler J.R., Hanash S.M.;
"Nm23-H1 mutation in neuroblastoma.";
"Nm23-H1 mutation in neuroblastoma.";
Nature 370:335-336(1994).
-!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
                  CTL-
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3D-structure; Anti-oncogene; ATP-binding; Cell cycle;
Direct protein sequencing; Disease mutation; Kinase; Magnesium;
Metal-binding; Nuclear protein; Nucleotide metabolism;
     ran 2., seresiora 2.0., on D.x., Zhang D., Lieberman J.;
"Tumor suppressor NM23-H1 is a granzyme A-activated DNase durin
mediated apoptosis, and the nucleosome assembly protein SET is
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GO; GO: 0005524; F:ATP binding; NAS.
GO; GO: 0004536; F:deoxyribonuclease activity; IDA.
GO; GO: 0004536; F:magnesium ion binding; IDA.
GO; GO: 0000287; F:magnesium ion binding; IDA.
GO; GO: 00004550; F:nucleoside-diphosphate kinase activity; NAS.
GO; GO: 0009142; P:nucleoside triphosphate biosynthesis; NAS.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as long as its content is in no way modified
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EMBL; X75598; CAA53270.1; -; Genomic_DNA.
EMBL; X73066; CAA51527.1; -; mRNA.
EMBL; BC000293; AAH00293.1; -; mRNA.
EMBL; BC018994; AAH18994.1; -; mRNA.
PIR; A33386; A33386.
PDB; 1JXV; X-ray; A/B/C/D/E/F=1-152.
PDB; 1JXV; X-ray; A/B/C=1-152.
Aarhus/Ghent-2DPAGE; 4115; IEF.
OGP; P15531; -.
PMMA-2DPAGE; P15531; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   different tumors.
SIMILARITY: Belongs to the NDK family.
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Zhang D
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Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
Oh D.Y
    F.J., Oh
NM23-H1
                                                                    112:659-672 (2003)
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Beresford P
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae,
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Ensembl; ENSG0000011052; Homo sapiens.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0016740; F:rucleoside-diphosphate kinase activity; IEA.

GO; GO:0006241; P:CTP biosynthesis; IEA.

GO; GO:0006183; P:GTP biosynthesis; IEA.

GO; GO:0006228; P:UTP biosynthesis; IEA.

InterPro; IPR001564; NDK.

InterPro; IPR012005; NDK-2.
        Pros-phosphohistidine intermediate.
Substrate ATP/NDP ribose.
Substrate ATP/NDP base.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP base.
Substrate ATP/NDP ribose.
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Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar
Korn B., Zuo D., Hu Y., LaBaer J.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR542104; CAG46901.1; -; mRNA.
EMBL; CR542115; CAG46912.1; -; mRNA.
                                                                                                                                                                                                                        Length 152;
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binding.
  Phosphorylation;
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ilarity 94.1%;
Conservative
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OGFGK3;
05-JUL-2004 (TrEMBLrel. 27
05-JUL-2004 (TrEMBLrel. 27
10-MAY-2005 (TrEMBLrel. 30
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Nucleotide-binding;
ACT_SITE 118
BINDING 12
BINDING 60
BINDING 88
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143; Conser
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homi
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        PRINTS; PR01243; NUCDPKINASE.
SMART; SM00562; NDK; 1.
PROSITE; PS00469; NDP_KINASES; 1.
SEQUENCE 152 AA; 17149 MW; AAE9C0DF63CB70A1
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Poustka A., Albert R., Moosmayer P., Schupp I.
Mewes H.W., Weil B., Amid C., Osanger A., Fobo
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ
EMBL; CR858425; CAH90654.1; -; mRNA.
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GO; GO: 0016301; F: kinase activity; IEA.
GO; GO: 0004550; F: nucleoside-diphosphate kis
GO; GO: 0016740; F: transferase activity; IEA.
GO; GO: 0006241; P: CTP biosynthesis; IEA.
GO; GO: 0006183; P: GTP biosynthesis; IEA.
GO; GO: 0006228; P: UTP biosynthesis; IEA.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
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Mismatches
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PRINTS; PR01243; NUCDPKINASE
ProDom; PD001018; NDK; 1.
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ilarity 94.1%;
Conservative
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94.1%;
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Submitted (Nov
EMBL; CR858425; C
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PROSITE; PS00
Hypothetical
SEQUENCE 15
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QSRC56;
01-FEB-2005
01-FEB-2005
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PAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structure.";
Biochemistry 37:13958-13967(1998).
-!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ή.
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98434367; PubMed=9760230; DOI=10.1021/bi9808538; Abdulaev N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L., Yakhyaev A.V., Tordova M., Gaidarov I.O., Popov V.I., Fujiwara J.H Chinchilla D., Eisenstein E., Gilliland G.L., Ridge K.D.; "Nucleoside diphosphate kinase from bovine retina: purification, subcellular localization, molecular cloning, and three-dimensional
                                                                                                                                                                                                                                                                                                                                                           SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pros-phosphohistidine intermediate.
Substrate ATP/NDP ribose.
Substrate ATP/NDP base.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP base.
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metabolism;
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                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom:
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia,
Pecora; Bovidae; Bovinae; Bos.
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PROTEIN SEQUENCE, NUCLEOTIDE SEQUENCE, CATALYTIC ACTIVITY, SUBCELLULAR LOCATION, BLOCKAGE OF THE N-TERMINUS, AND X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
TISSUE=Retina;
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PDB; 1BHN; X-ray; A/B/C/D/E/F=1-151.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
Pfam; PF00334; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
SMART; SM00562; NDK; 1.
PROSITE; PS00469; NDP KINASES; 1.
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                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Nucleoside diphosphate kinase NBR-A (EC 2.7.4.6)
kinase NBR-A)
                                                  166
                                                                             52
                                                                 PTM: The N-terminus is blocked. SIMILARITY: Belongs to the NDK family
                                                   DSVKSAEKEISLWFQPEELVEYKSCAONWIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP + nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other than ATP.

CATALYTIC ACTIVITY: ATP + nucleosid nucleoside triphosphate.

COFACTOR: Magnesium (By similarity) SUBUNIT: Homohexamer.

SUBCELLULAR LOCATION: Cytoplasmic a
                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                         TGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNI
                                                                                                                                                                                                                                AGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNI
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                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE, NUCLEOTIDE SEQUENCE, CATALYTIC ACTIVITY, SUBUN SUBCELLULAR LOCATION, BLOCKAGE OF THE N-TERMINUS, AND X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        triphosp
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98434367; PubMed=9760230; DOI=10.1021/bi980853s; Abdulaev N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L., Yakhyaev A.V., Tordova M., Gaidarov I.O., Popov V.I., Fujiwara JChinchilla D., Eisenstein E., Gilliland G.L., Ridge K.D.; "Nucleoside diphosphate kinase from bovine retina: purification, subcellular localization, molecular cloning, and three-dimensior
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                                                                                                                                                                                                                                                                                                                            (NDK NBR-B)
                                                                                                                                                                        151;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           structure.";
Biochemistry 37:13958-13967(1998).
-1- FUNCTION: Major role in the synthesis of nucleoside other than ATP.
                                                                                                                                                                       Length
 ribose
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                                                                                                                                                                       Score 750; DB 1; Pred. No. 2.1e-62; Hismatches 5;
                                                                                                                                                           AAD80B21137EA4E1
 Substrate ATP/NDP Substrate GDP N2.
                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Nucleoside diphosphate kinase NBR-B (EC 2.7.4
kinase NBR-B).
                                                                                                                                                                                                                                                  166
                                                                                                                                                                                                                                                        SVKSAEKEISLWFOPEELVEYKSCAONWIYE
                                                                                                                                                           MW;
                                                                                                                                                                       Query Match
Best Local Similarity 92.7%;
Matches 140; Conservative
1114
151
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16
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 TISSUE=Retina;
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SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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PDB; 1BE4; X-ray; A/B/C=1-151.

InterPro; IPR001564; NDK.

InterPro; IPR012005; NDK-2.

R InterPro; IPR012005; NDK; 1.

PIRSF; PIRSF000735; NDK; 1.

R PRINTS; PR01243; NUCDPKINASE.

R PRODOM; PD001018; NDK; 1.

R SMART; SM00562; NDK; 1.

R PROSITE; PS00469; NDP KINASES; 1.

R Magnesium; Metal-binding; Nuclear protein; Nucleotide metabolism; Nucleotide-binding; Phosphorylation; Transferase.

I INIT MET 0 0 0

I NUT MET 117 117 Pros-phosphohistidine intermediate.

PROSITE 117 117 Substrate ATP/NDP ribose.
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                                           plasma
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Pred. No. 2.6e-62
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Mismatches
                                             and
                                                       membrane.
PTM: The N-terminus is blocked.
SIMILARITY: Belongs to the NDK family
+ nucleoside
      nucleoside triphosphate.
COFACTOR: Magnesium (By similarity)
SUBUNIT: Homohexamer.
SUBCELLULAR LOCATION: Cytoplasmic a
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ilarity 92.7%;
Conservative
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InterPro; IPR012005; NDK-2.
Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
SMART; SM00562; NDK; 1.
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diphosphate kinase
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ilarity 92.1%;
Conservative
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                                                                                                                                                    NUCLEOTIDE SEQUENCE [MRNA]
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(TrEMBLrel.
(TrEMBLrel.
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140; Conser
                                                                                                                     NCBI_TaxID=9615;
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Q50KA8 CANFA
Q50KA8;
13-SEP-2005
13-SEP-2005
13-SEP-2005
NM23-C2.
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  Nucleoside
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Best Local
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IIHGS
  TGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD
                       IHGSD
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TISSUE=Lymphoid;

Yu J., Meng Y., Wang Z., Hansen C., Li C., Moore S.;

Yu J., Meng Y., Wang Z., Hansen C., Li C., Moore S.;

Yu J., Meng Y., Wang Z., Hansen C., Li C., Moore S.;

Yu J., Meng Y., Wang Z., Hansen C., Li C., Moore S.;

Thalysis of sequences obtained from constructed full-length bovine cDNA libraries.";

Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; AY911378; AAW82141.1; -; mRNA.

R SMR; Q56JV4; 5-152.

R SNR; Q56JV4; 5-152.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0016301; F:Kinase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0006241; P:CTP biosynthesis; IEA.

R GO; GO:0006289; P:UTP biosynthesis; IEA.

R GO; GO:0006289; P:UTP biosynthesis; IEA.

R InterPro; IPR012005; NDK-2.

INTERPRO; IPR012005; NDK-2.
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Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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                    AGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNI
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(TrEMBLrel. 30, Last sequence update)
(TrEMBLrel. 30, Last annotation update)
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Pred. No. 3.3e-62
5; Mismatches
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, Last sequence update)
, Last annotation update)
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                                                                                   SVESAEKEIALWFRPEELVNYKSCAQNWIYE
                                                                      SVKSAEKEISLWFQPEELVEYKSCAQNWIYE
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ilarity 92.1%;
Conservative 6
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NUCDPKINASE
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ses 140; Conser
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10-MAY-2005
10-MAY-2005
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13-SEP-2005
13-SEP-2005
13-SEP-2005
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PIRSF;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae
                                                                                                                                                                                    K., Miyoshi
                                                                                                                                                                                                                                                                                                                                                                                   nucleoside triphosphate.

COFACTOR: Magnesium (By similarity).

SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A A3B3, A2B4, AB5, B6). Interacts with SET (By similarity).

SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).

SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                          Takahashi M., Une R., Fukushima K., Fujiki M., Misumi K., Miyosh Endo Y., Oishi A., Akuzawa M.;

"Molecular cloning of canine nm23 cDNAs and their expression in and tumor tisuues.";

Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Major role in the synthesis of nucleoside triphosp other than ATP (By similarity).

-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intermediate
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PROSITE; PS00469; NDP_KINASES; 1.
ATP-binding; Kinase; Magnesium; Metal-binding; Nuclear protein;
Nucleotide metabolism; Nucleotide-binding; Phosphorylation;
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669D444D69380FE6 CRC64;
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Last sequence update)
Last annotation update)
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Pred. No. 6.3e-62;
Mismatches
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NDK
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Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                        Takahashi M., Une R., Fukushima K., Fujiki M., Misumi K., Miyoshi N Endo Y., Oishi A., Akuzawa M.;

Endo Y., Oishi A., Akuzawa M.;

"Molecular cloning of canine nm23 cDNAs and their expression in nor and tumor tisuues.";

Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; AB207045; BAD97838.1; -; mRNA.

SMR; Q50KA8; 2-152.

InterPro; IPR012005; NDK.

InterPro; IPR012005; NDK-2.

Pfam; PF00334; NDK; 1.

R PIRSF; PIRSF000735; NDK; 1.

R PRINTS; PR01243; NUCDPKINASE.

R PRODOM; PD001018; NDK; 1.
                                                                            K., Miyoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Hystricognathi; Caviidae; Cavia.
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TISSUE=Cardiac endothelium;

TISSUE=Cardiac endothelium;

Buxton I.L.O., Kaiser R.A., Oxhorn B.C., Cheek D.J.;

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Belongs to the NDK family.

EMBL; AY017306; AAK00527.1; -; mRNA.

HSSP; P15531; 1JXV.

SMR; Q99N12; 5-153.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004550; F:hucleoside-diphosphate kinase activity; IEA.

GO; GO:0006241; P:CTP biosynthesis; IEA.
                                                                                                                                                                                                                                                                    152;
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q99N12_CAVPO PRELIMINARY; PRT; 153 AA.
Q99N12;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nucleoside diphosphate kinase A.
                                                                                                                                                                                                                                                                 Score 735; DB 2; I
Pred. No. 5.5e-61;
); Mismatches 5;
                                                                                                                                                                                                                                   1.
923DA489B37C19C6
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                                                                                                                                                                                                                      SMART; SM00562; NDK; 1.
PROSITE; PS00469; NDP_KINASES;
SEQUENCE 152 AA; 17366 MW;
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ilarity 90.1%;
Conservative 10
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TISSUE=Cardiac endothelium;
Buxton I.L.O.;
                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                             l Similarity
137; Conser
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NCBI_TaxID=10141;
[1]
                               Canis.
NCBI_TaxID=9615;
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:imates; Catarrhini; Hominidae;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp468E0516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bahr A., Lauber J., Mewes H.W., well E., .....

Han M., Wiemann S.;

Submitted (NOV-2004) to the EMBL/GenBank/DDBJ datak
EMBL; CR857184; CAH89484.1; -; mRNA.

SMR; O5RFH3; 2-152.

GO; GO:00065524; F:ATP binding; IEA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:00064550; F:nucleoside-diphosphate kinase act

GO; GO:0016740; F:kransferase activity; IEA.

GO; GO:0006241; P:CTP biosynthesis; IEA.

GO; GO:000628; P:UTP biosynthesis; IEA.

GO; GO:000628; P:UTP biosynthesis; IEA.

InterPro; IPR001564; NDK.

InterPro; IPR001505; NDK-2.

R Pfam; PF00334; NDK; 1.
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                                                                                                                                                                                                       Score 732.5; DB 2;
Pred. No. 9.5e-61;
; Mismatches 4;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Mammalia; Eutheria; Euarchontoglires; Primates;
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Pred. No. 1e-60;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                166
                                                                                                                                                                                                                                                                                                                                                                                                                                                153
                                                                                                                                                                                                                                                                                                                                                                                                            J., Mewes H.W., Weil B., S.;
GO, GO:0006183; P:GTP biosynthesis; I)
GO; GO:0006228; P:UTP biosynthesis; I)
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
SMART; SM00562; NDK; 1.
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                                                                                                                                                                       MM;
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PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 83.6%;
11 Similarity 90.1%;
137; Conservative 1
                                                                                                                                                                                                       ch 83.6%;
il Similarity 90.8%;
139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Heart;
The German cDNA Consortium;
Bahr A., Lauber J., Mewes H
                                                                                                                                                                         17198
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DD 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152

Search completed: December 16, 2005, 16:37:01 Job time : 155.472 secs

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5.1.6 Compugen Ltd. version - 2005 GenCore (c) 1993 Copyright

sw model using protein search, OM protein

16:31:59 2005, 16, December Run on:

tes/sec conds updat Se ; Search time 34.4528 (without alignments) 398.346 Million cell up

... WFQPEELVEYKSCAQNWIYE US-10-074-694 876 score: Title: Perfect so Sequence:

1 QSQPAVKPCHLKGTMANSER...

166

BLOSUM62 Gapop 10.0 table Scoring

0.5 572060 segs, 82675679 Gapext

Searched

residues

572060 hits satisfying chosen parameters: of Total number

2000000000 length: length: sed 0B 0B Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Patents Issued Database

/cgn2_6/ptodata/1/iaa/5_COMB.pep:*/cgn2_6/ptodata/1/iaa/6_COMB.pep:*/cgn2_6/ptodata/1/iaa/H_COMB.pep:*/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*/ H 2 W 4 W 0

rinted No. is the number of results predicted by chance to have greater than or equal to the score of the result being ps derived by analysis of the total score distribution. score gand is Pred.

SUMMARIES

		de				
Result No.	Score	Query Match	Length	DB	ΩI	Description
1	79	~	ı	2	US-09-335-948-5	Sequence 5, Appli
8	G		8	7	-07-806-	e 1,
ım	. IO		W	7	US-08-713-825-4	4,
4	. ID	10	152	7	US-09-199-842-4	4, Appl
· m	·ιΛ	10	Ŋ	~	0	4, App
9	10	10		~	US-09-460-532-4	4, Appl
7	ın	10	Ŋ	~	-09-53	933, Ap
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g	m	~	176	~	US-07-806-932B-3	3, Appl
10	\sim	~	Ŋ	-4	-08-713-825-	_
11	\sim	~	S	~	-09-199-842-	5, Appl
12	N	~	S	7	4	1, Appl
13	N	~	ហ	~	-09-460-532-	equence 5, Appl
4	N	~	ហ	~	-09-538-09	987, Ap
15	47.	\sim	9	, - 1	-08-667-023-	equence 2, Appl
16	•	ς.	9	m	2	equence 3, Appl
17	47.	~	9	7	-199-842-	3, Appl
18	47.	~	9	~	-09-460-53	equence 3, Appl
19	54	_;	117	7		5323, A
20	ന	6	S	7	-09-248-79	equence 18029,
21	\sim	<u>.</u>	151	~	US-09-183-861-20	20, App
22	N	0	151	~	US-09-022-765-20	equence 20, App
23	N	0	151	~	-551-974A-2	equence 20, App
24	N	ö	151	7	5-501A-	20, App
25	N	0	151	7	-639-206A-2	Sequence 20, Appl
26	N	0	151	7	4-923-2	equence 20, App
27	N	0	151	7	US-08-798-841-20	Sequence 20, Appl

Sequence 491, App Sequence 1, Appli	Sequence 1, Appli	App	23, A	Sequence 59, Appl	, Apr	216,	Sequence 91, Appl	91, Ag	639,	3645,	Sequence 6000, Ap	ď	'n	Apr	-	9
-09-538-0 -08-713-8	-09-199-	US-09-460-532-1	US-09-538-092-823	US-09-443-184-59	US-10-227-035-4	09-134-0	US-09-358-972-91	US-09-790-417-91	09-583-110-363	09-107-433-3	09-107-5	US-09-937-296-1	06-60	US-09-937-296-2	US-09-252-991A-22989	-352-7
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ALIGNMENTS

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Sequence 5, Application US/09335948

Sequence 5, Application US/09335948

Patent NO. 6229198

GENERAL INFORMATION:

APPLICANT: National Institutes of Health
APPLICANT: Charles R. King

APPLICANT: Patricia S. Steeg

APPLICANT: Lance A. Liotta

TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN

TITLE OF INVENTION: AND ANTIBODIES THEREFOR

TITLE OF INVENTION: AND ANTIBODIES THEREFOR

FILE REFERENCE: 14014.0321

CURRENT APPLICATION NUMBER: US/09/335,948

CURRENT PILING DATE: 1999-06-18

PRIOR FILING DATE: 1995-06-07

PRIOR PILING DATE: 1991-12-11

PRIOR PILING DATE: 1991-12-11

PRIOR PILING DATE: 1999-10-18

NUMBER OF SEQ ID NOS: 6

SECOTOR NOTE: NUMBER: OT/422,801

PRIOR FILING DATE: 1989-10-18

NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 794; DB 2; 1
Pred. No. 2.4e-85;
1; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match
Local Similarity 91.5%;
nes 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CRGANISM: Homo Sapiens
US-09-335-948-5
                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 5
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 150
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RESULT 2
US-07-806-932B-1
; Sequence 1, Application US/07806932B
; Patent No. 6423836
; GENERAL INFORMATION:



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STATE:

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135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09199842

Patent No. 6087125

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LI
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, In
                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
              SEE: Incyte Pharmaceuticals, : 3174 Porter Drive Palo Alto
                                                                                                                                                           SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,825
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.6%;
ilarity 94.1%;
Conservative
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Palo Alto
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amino acid
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468542
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Best Local Similarity
Matches 143; Conser
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                                                                   COUNTRY: U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY:
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CITY: Pa
STATE: C
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                                         CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 184;
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                  AND USE OF HUMAN PROTEIN AND ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIQUGRNI IHGSDSVKSAEKEI SLWFQPEELVEYKSCAQNWIYE
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Phillip R.
NOVEL HUMAN NM23-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
10;
                                                                                              GILFILLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 794; DB 2;
Pred. No. 2.4e-85;
Mismatches 1
                                                                                                                                                                                                                                                         SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/806,932B
FILING DATE: 11 december 1991
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                               NAME: CAPELLO, SUSAN A.
REGISTRATION NUMBER: 34,560
REFERENCE/DOCKET NUMBER: 469200-72
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -32
                                                                                             BAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IARACTERISTICS:
184 AMINO ACID RESIDUES
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/422,801
FILING DATE: 18 october 1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08713825
; Patent No. 5874285
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN NI
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE: HUMAN NM 23-H28
PUBLICATION INFORMATION: 1: FROM
   AL.
PRODUCTION
                               HUMAN NM23
THEREFOR
                                                                                       S: CARELLA, BYRNE, F
S: CECCHI & STEWART
6 BECKER FARM ROAD
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larity 91.5%;
Conservative
           TITLE OF INVENTION: PROF
TITLE OF INVENTION: HUM
TITLE OF INVENTION: THEN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                    APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN
                                                                                                                                                     NEW JERSEY
                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: DW4.V2
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                                                                                                                                                                  USA
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                                                                                      ADDRESSEE:
ADDRESSEE:
                                                                                                                                                                 COUNTRY: UN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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APPLICANT:
TITLE OF I
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LENGTH:

US-08-713-825-4

RESULT

81

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123

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141

d d

Query Match

Best Local Matches 19

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15 MANSERTFIAIKPDĠVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF 75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS .. 0 Length 152; Indela Olga Phillip R. NOVEL HUMAN NM23-LIKE PROTEIN ...6 Score 759; DB 1; Pred. No. 2.4e-81; Mismatches 166 STATE:
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TWOTTER: IBM COMPAtible

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